

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 124765

To: Elizabeth McElwain

Location: REM-2A11/2C18

Art Unit: 1638

Thursday, June 24, 2004

Case Serial Number: 10/069772

From: Beverly Shears Location: Remsen Bldg.

RM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes				
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Matches 377
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FEBS Lett. 462:249-253(1999).
EMBL; AJ245938; CAB64256.1; -.
GO; GO:0016491; F:oxidoreductase act:
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
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SEQUENCE 377 AA; 43615 MW; 1CBF76
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae;

Calendula.
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MEDLINE=20086417; PubMed=10622705;
Fritsche K., Hornung B., Peitzsch N., Renz A., Feussner I.;
Fischation and characterization of a calendic acid producin
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 MGAGGRMSDPSEGKNILERVPVDPPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAYV
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Q7XA13;

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01-OCT-2003 (TrEMBLrel. 25, Created)

01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Delta12-fatty acid acetylenase.

Helianthus annuus (Common sunflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

Spermatophyta; Asterales; Asteraceae; Asteroideae; Heliantheae;
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MEDLINE=22674157; PubMed=12787248;

MEDLINE=22674157; PubMed=12787248;

Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.

"Fungal responsive fatty acid acetylenases occur

"Fungal responsive fatty acid acetylenases occur

evolutionarily distant plant families.";

Plant J. 34:671-683(2003).

EMBL; AY166773; AA038032.1; -.

SEQUENCE 377 AA; 43750 MW; 832C8A129C6C2A55 C
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KGAAWVTCMYLIPVLGVHMFFVLITYLHHTHLSLPHYDSTEWNWIRGALSTIDRDFGFLN
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Q7XA08 PRELIMINARY; PRI Q7XA08; 01-OCT-2003 (TrEMBLrel. 25, Creat 01-OCT-2003 (TrEMBLrel. 25, Last 01-OCT-2003 (TrEMBLrel. 25, Last Delta12-fatty acid acetylenase (i Helichrysum bracteatum.

Last sequence update)
Last annotation update)

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Best Local Similarity
Matches 300; Conserv
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SEQUENCE FROM N.A.

MEDLINE=22674157; PubMed=12787248;
Cahoon B.B., Schnurr J.A., Huffman E.A., Minto R.J.

Cahoon B.B., Schnurr J.A., Huffman E.A., Minto R.J.

Pungal responsive fatty acid acetylenases occur vevolutionarily distant plant families.";

evolutionarily distant plant families.";

Plant J. 34:671-683(2003).

EMBL; AY166776; AAO38035.1; -.

NON_TER 326 326

SEQUENCE 326 AA; 37861 MW; D3C65BAD9EF25783 CI
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Delta12-fatty acid acetylenase (Fragment).
Rudbeckia hirta.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
Rudbeckia.
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Q7XA10;
01-OCT-2003
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Pred. No. 3.6e-134;
1; Mismatches 15;
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                                                                  SEQUENCE FROM N.A.

MEDLINB=22674157; PubMed=12787248;
Cahoon E.B., Schnurr J.A., Huffman E.A., Mi
"Fungal responsive fatty acid acetylenases
evolutionarily distant plant families.";
Plant J. 341671-683(2003).
                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae;
                                                                                                                                                                                                          01-OCT-2003 (TREMBLrel. 25, Created)
01-OCT-2003 (TREMBLrel. 25, Last sequence update)
01-OCT-2003 (TREMBLrel. 25, Last sanotation update)
Deltal2-fatty acid acetylenase (Fragment).
Dimorphotheca sinuata (African daisy)
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MEDLINE=2674157; PubMed=12787248;
Cahoon E.B., Schnurr J.A., Huffman E.A., Mi
"Fungal responsive fatty acid acetylenases
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                                                                                                                                                   NCBI_TaxID=112408;
                                                                                                                                                                Dimorphotheca
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326 AA;
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Pred. No. 5.7e-131;
vigmatches 21;
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EMBL; Y10283; CAA76156.1; -
GO; GO:0016491; F:oxidoreductase ac
InterPro; IPR005804; FA desat fam.
Pfam; PP00487; FA desaturase; 1.
ProDom; PD001081; FA desat_fam; 2.
SEQUENCE 374 AA; 43323 MW; 776.
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MEDLINE=98239771; PubMed=9572738;
Lee M., Lenman M., Banas A., Bafor M.,
Nilsson R., Liljenberg C., Dahlqvist A
Green A., Stymne S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Delta 12 fatty acid epoxygenase.
Crepis palaestina.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster
campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Cre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green A., Stymme S.;
"Identification of Non-Heme Diiron Proteins That Catalyze Triple Bond and Epoxy Group Formation.";
Science 280:915-918(1998).
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01-AUG-1998
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"Fatty acid desaturases from borage.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ dat
EMBL; AF074224; AAC31698.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.
ProDom; PD001081; FA desat fam; 2.
SEQUENCE 383 AA; 44048 MW; 13DF2BD876E7E5EF (
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PRELIMINARY; PRT; 383 AA.

O82729;
O1-NOV-1998 (TrEMBLrel. O8, Created)
O1-NOV-1998 (TrEMBLrel. O8, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 24, Last annotation update)
O1-UN-2003 (TrEMBLrel. 24, Last annotation update)
Delta-12 fatty acid degaturage.
Borago officinalis (Bourrache) (Borage).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Boraginaceae; Borago.

NCBI TaxID=1383;
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Sayanova O., Shewr
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ECIYIEPDEDSEHKGVFWY
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                                                                                                                                                                                                                                                                                                                                                                                                             TVGLLLHSALLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKRSGISWSSEYLNNPPGRVL
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                                                                                                                                FGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK
                                                                                                        YGFLNKVLHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGDYYQCDRTPVFKAMYREVK
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Pred. No. 1.2e
52; Mismatches
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13DF2BD876E7E5EF
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RESULT 9
Q9LLL7
ID Q9LL
AC Q9LL
DT 01-0
DT 01-0
DT 01-J
DT 01-J
DT 01-J

Q9LLL7 Q9LLL7; Q9LCT-2000 01-OCT-2000 01-JUN-2003

PRELIMINARY;

383

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2000 (TrEMBLrel. 15, Cr 2000 (TrEMBLrel. 15, La 2003 (TrEMBLrel. 24, La fatty acid desaturase.

Last sequence update)
Last annotation update)

Created)

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Best Local S
Matches 241
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EMBL; AF52553; AAN87573:1; --
GO; GO:0016491; Froxidoreductase acti.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00479; FA_desaturase; 1.
ProDom; PD0041081; FA_desat_fam; 2.
SEQUENCE 383 AA; 44152 NW; F5D061
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Q8GZC3;
Q8GZC3;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 24, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Delta 12 Oleic acid desaturase FAD2.
Vernicia fordii (Tung) (Aleurites Fordii).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
seurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Aleuritideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dyer J.M., Chapital D.C., Kuan J.-C.W., Mullen R.T., Turner C., McKeon T.A., Pepperman A.B.; "Molecular Analysis of a Bifunctional Fatty Acid Conjugase/Desaturase from Tung. Implications for the Evolution of Plant Fatty Acid Diversity.";
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PubMed=12481086;
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                                                                                                        FGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK
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YGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPFYKAMWREAK
                                                                                                                                                                                                                 TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK
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                                                    ЕСІУІЕРДЕДІВНІКСУЕМУНК 376
                                                                                                                                                                                                                                                                                                                                      TLTITLTLGWPLYLAFNVSGRPYDRFACHYDPYGPIYTDRERTEIYISDAGVLAVTFGLY
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ECIYVEADDGDESKGVYWYNK
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Pred. No. 7.2e-
61; Mismatches
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F5D06112C313B3CB CRC64;
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e-112;
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Q8W2F

Q8W2F

ID Q8W2F

AC Q8W2F

AC Q8W2F

AC Q8W2F

O1-MA

DT 01-MA

DT 01-JU

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GN FAD2-

OS Helia

OC Sukar

OC Campaa

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Best Loc
Matches
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Jin U.H., Chung C.H.;

Jin U.H., Chung C.H.;

"Molecular characterization of a omege-6 fatty acid
sesame (Sesamum indicum L.) seeds.";

Submitted (CCT-1999) to the EMBL/GenBank/DDBJ datak

EMBL; AF192486; AAF80560.1; -.

GO; GO:0016491; F:oxidoreductase activity; IEA.

InterPro; IPR005804; FA, desat fam.

Pfam; PF00487; FA, desat fam; 2.

SEQUENCE 383 AA; 44265 MW; F324272C3D57BBF5 CRO
                                                                                                                                                                                                                  Helianthus annuus (Common sunflower).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Aggroliophyta; Streptophyta; core eudicots; asterids; Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TIEMBLIE). 20, Created)
01-MAR-2002 (TIEMBLIE). 20, Last sequence up
01-JUN-2003 (TIEMBLIE). 24, Last annotation
Delta-12 oleate desaturase (EC 1.3.1.35).
                                       "Spatial and temporal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8W2F0
                                                                                       STRAIN-HA89;
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8W2F0;
                  desaturase
                                                                                                                                                                    NCBI_TaxID=4232;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Lamiales; Pedaliaceae; Sesamum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECIYIEPDEDSEHKGVFWY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGVLNKVFHNITDTHVTHHLFSTMPHYHAMEATKAIKPILGQYYQFDGTPFYKAMMREAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVALVKGLAWLVCVYGVPLLIVNGFLVLITFLOHTHPSLPHYDSSEWDWLRGALATVDRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVAYVEYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECLYVEPDESTPDKGVFWY
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               genes
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               (FAD2)
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Sperling P., Luchs W., Heinz E.;
1. regulation of three different microsomal oleate
1. regulation of three and high-oleic varieties of
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Pred. No. 9.6e
50; Mismatches
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Query Match
Best Local S
Matches 241
                                                                                        Wang X., Lichter A., Prusky D.;
"Isolation of a cDNA Clone Encoding an Avocado (1)
Delta-12 Fatty Acid Desaturase.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ dat
EMBL; AY057406; AAL23676-1; -.
GO; GC:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desat_fam; 2.
SEQUENCE 382 AA; 43492 MW; 8323B053D866B3B8 (
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Q8H2C3;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; magnoliids;
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01-MAR-2003 (TYEMBLrel. 23, Last sequence up
01-UN-2003 (TYEMBLrel. 24, Last annotation
Delta-12 fatty acid desaturase.
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Mol. Breed. 8:159-168(2001).
EMBL; AF251843; AAL68982.1; -.
GO; GO:0016491; F.oxidoreductase activity;
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Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
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                        66.4%;
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8323B053D866B3B8
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Best Local Similarity
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Q9SP28;
01-MAY-2000
01-MAY-2000
01-JUN-2003
                                                                                                                                                                                                                                                                                                                Hage T.G., Seither C., Hildebrand D.;
"Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.
encoding a microsomal oleate desaturase (FAD2) (accession nos.
AF188263 and AF188264) and functional expression in Saccharomy.
cerevisiae (PGR00-035).";
Plant Physiol. 122:1457-1457(2000).
EMBL; AF188264; AAF04094.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desat_fam.
Pfam; PF00487; FA_desat_fam.
                                                                                                                                                                                                                                                               Oxidoreductase.
SEQUENCE 383
                                                                                                                                                                                                                                                                                                ProDom; PD001081; FA_desat_fam; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10759541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=83960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vernonia galamensis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Vernonieae;
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                        LTISFIFYYLATNYIPLLPHPLSYVAWPVYWIFQGCVLTGVWVIAHECGHHAFSDYQWLD
                                                            LIVAYVFYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLID
                                                                                                   MGAGGRMSNPPKDEKKAEHEALQRVPYQKPPFTVGDIKKAIPPHCFNRSVIRSFSYVVYD
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                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                               44330 MW;
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Last annotation update)
(EC 1.3.1.35).
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                                                                                                                                                                              Score 1359.5;
Pred. No. 1.9e
61; Mismatches
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es 73;
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DENVZE9
ID WAZE
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DT 01-MJ
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                                                                                                                                                                                                                                                                                                                                                              Matches 239;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF251844; AAL68983.1; -. GO; GO:0016491; F:oxidoreductase al InterPro; IPR005804; FA_desat_fam. Pfam; PF00487; FA_desaturase; 1. ProDom; PD001081; FA_desat_fam; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAD2-3.
Helianthus annuus (Common sunflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
Helianthus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martinez-Rivas J.M., Sperling P., Luehs W., Heinz E.; "Spatial and temporal regulation of three different micr desaturase genes (FAD2) from normal-type and high-oleic sunflower (Helianthus annuus L.)."; where the sunflower (Helianthus annus L.)."; "Read. 8:159-168 (2011).
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase.
SEQUENCE 382 AA;
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                                                                                                                                                                                                                                                                                                        1 MGAGGRMSDPS----EGKNILER-VPVDPPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
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                                     TVGLILHSALLVPYFSWKYSHRRHHSNTGSIEHDEVFVPKLKSSVRSTAKYLNNPPGRIL
                                                                                                                                           IVGFVLHSALLTDYFSWKYSHRNHHANTNSLDNDEVYIDKRKSKVKIYSKLLNNDDGRVF
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LLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRD
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                                                                                                                                                                                                                                                                               MGAGGRMSSPNGKEKDGPKPLERALHEKPPFTVGDIKKVIPPHCFKRSVIRSFSYVVYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                             44004 MW;
                                                                                                                                                                                                                                                                                                                                                                                 66.3%;
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0, Last sequence upo
4, Last annotation of the (EC 1.3.1.35).
                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                              Score 1357; DB 10;
Pred. No. 3.1e-109;
9; Mismatches 75;
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DT 01-MB

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Best Local Similarity
Matches 237; Conserv
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Q9SP29;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hage T.G., Seither C., Hildebrand D.;
"Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.
encoding a microsomal oleate desaturase (FAD2) (accession nos.
AF188263 and AF188264) and functional expression in Saccharomyces
cerevisiae (PGR00-035).";
Plant Physiol. 122:1457-1457(2000).
EMBL; AF188263; AAF04093.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005804; FA desat fam.
PFEM; PF00487; FA desaturase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vernonia galamensis.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Cichorioideae; Vernonieae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Delta-12 oleate desaturase (EC 1.3.1.35).
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                                                                                            DFGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREA
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PIR; T10480; T10480.

GO; GO:0016491; F:oxidoreductase ac Interpro; IPR005804; FA desat fam. Pfam; PF00487; FA desaturase; 1.

Probom; PF00487; FA desaturase; 2.

SEQUENCE 383 AA; 44101 MW; F170
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    Officinalis calendulic acid desaturase.

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New nucleic acid sequence encoding Calendula officinalis calendulic acid desaturase, useful for e.g. producing transgenic plants having oil with an increased unsaturated fatty acid content,.

Claim 1c; Page 15-16; 22pp; German.

This invention describes a novel isolated nucleic acid sequence (I) encoding a Calendula officinalis calendulic acid desaturase polypeptide. The invention also describes (1) a process for producing unsaturated fatty acids, comprising introducing at least one copy of (I) or (II) into an oil-producing organism, growing the organism, isolating oil from the organism and releasing fatty acids from the oil, (2) a process for producing triglycerides with an increased unsaturated fatty acid content, comprising introducing at least one copy of (I) or (II) into an oil-producing organism, growing the organism and isolating oil from the organism and isolating oil from the organism; (3) a process for producing saturated fatty acids, comprising introducing at least one nonfunctional copy of (I) or (II) into an oil-producing at least one nonfunctional copy of (I) or (II) into an oilproducing organism, growing the organism, isolating oil from the organism

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                            29-MAR-1996;
                                                                                 14-FEB-1997;
                                                                                                                                      09-OCT-1997.
                                                                                                                                                                                            WO9737033-A1
                                                                                                                                                                                                                                               Crepis alpina
                                                                                                                                                                                                                                                                                                                          Crepis alpina
                                                                                                                                                                                                                                                                                                                                                                                Crepis alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
20-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW36793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW36793 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAKECIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVFTLVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYYLANTYIPLIPTPLAYLAMPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGAGGRMSDPSEGKNILERVPVDPPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVFHDVTHTHVLHHLISYIPHYHAKBARDAIKPVLGBYYKIDRTPIFKAMYRBAKECIYI
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                              delta 12 acetylenase; plant; yeast; acetylenic oating; plastic; lubricant; oilseed.
                                                                                                                                                                                                                                                                                                                                                                                delta 12 acetylenase
                              96SE-00001236
                                                                                 97WO-SE000247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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                                                                                                                                                                                                                                                                                                                                compound;
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RESULT 3
AAW79743
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AAW79743 standard; protein; 374

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AAW79743;

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Best Local S
Matches 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bafor M,
Sjoedahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New acetylase used for production of crepenynic derived from Crepis alpina; used for production suited for the production of coatings, plastics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LENM/)
(SJOE/)
(STYM/)
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(BANA/)
(DAHL/)
(GUMM/)
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 21; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-503117/46.
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LENMAN M.
SJOEDAHL S.
STYMNE S.
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BANAS A.
DAHLQVIST A.
GUMMESON P.
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                RVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAKECIYI
                                                                                                                                                                                                                                                              FYYLANTYIPLIFTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFV 120
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                                                                                                                   KGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLN
                                                                                                                                                                       LTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAA
                                                                                                                                                                                                                             LHSALLTPYFSWKYSHRNHHANTNSLDNDBVYIPKRKSKVKIYSKLLNNPPGRVFTLVFR
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EPEKGRESKGVYWYNK
                        EPDEDSEHKGVFWYHK 376
                                                                                                                                                          FTLGFPLYLFTNISGKKYERFANHFDPMSPIFKERERFQVLLSDLGLLAVLYGVKLAVAA
                                                                                                                                                                                                               LHSFLMTPYFSWKYSHRNHHANTNSLDNDEVYIPKSKAKVALYYKVLNHPPGRLLIMFIT 178
                                                  SVLHDVTHTHVMHILFSYIPHYHAKBARDAINTVLGDFYKIDRTPILKAMWRBAKECIFI
                                                                                                       KGAAWVTCIYGIPVLGVFIFFDIITYLHHTHLSLPHYDSSEWNWLRGALSTIDRDFGFLN
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S, Stymne
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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S;
                                                                                                                                                                                                                                                                                                                                                                                   79.9%;
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                                                                                                                                                                                                                                                                                                                                                                       Score 1636; DB 2;
Pred. No. 1.6e-158;
0; Mismatches 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid from linoleic acid of acetylenic fatty acid and lubricants.
                                                                                                                                                                                                                                                                                                                                                                                                Length 375;
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                                                                                                                                                             This is the amino acid sequence of a novel epoxygenase of a vernolic acid containing Crepis sp. (not crepts palaestina). It was deduced from cisclated cDNA clone CrepX (see AAM63102). The deduced sequence contains cisclated cDNA clone CrepX (see AAM63102). The deduced sequence contains cont
                                                                            Query Match
Best Local S
Matches 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1997;
15-APR-1997;
16-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated fatty acid epoxygenase gene - used particularly for transforming plants for producing modified oils for use in, e.g. coatings, resins, glues, plastics, surfactants or lubricants.
                                                                                                                                                                                                   be used in proor lubricants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-568734/48.
N-PSDB; AAV63102.
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mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;
vegetable oil; oilseed.
                                                                                                                                                           Sequence 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 29; Page 84-86; 150pp; English.
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(STYM/)
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                                                                                                 Similarity
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                  MGAGGRMSDPSEGKNILERVPVDP-PFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAY 59
Green A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              delta-12-epoxygenase.
                                                                              Conservative
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97AU-00006226.
97US-0043706P.
97US-0050403P.
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293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by GTN"
309. .313
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15-APR-1997;
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20-JUN-1997;
                      New isolated fatty acid epoxygenase gene - used particularly transforming plants for producing modified oils for use in, coatings, resins, glues, plastics, surfactants or lubricants
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N-PSDB; AAV63101.
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                                                          Vernonia galamensis
                                                                                              Vernonia galamenensis; fatty acid desaturase; epoxidising enzyme; expression; chimeric gene; recombinant enzyme.
                                                                                                                                                           Vernonia galamenensis fatty acid epoxidising enzyme
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10-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is Vernonia galamenensis fatty acid epoxidising enzyme. The present invention also describes: (i) Vernonia galamenensis fatty acid desaturase; (ii) chimeric genes comprising the fragments linked to regulatory sequences; and (iii) transformed host cells containing the chimeric genes. The DNA's from the present invention can be used to alter levels of expression of the enzymes in transformed host cells or to produce the recombinant enzymes by transformation of microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding Vernonia galamenensis fatty acid desaturase and fatty acid epoxidising enzyme - used to alter levels of expression of the enzymes transformed host cells or to produce recombinant enzymes.
                                                                                                   AAY72825 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Col 29-32; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-059065/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAKECIYIEPDEDSEHKGV
                                                                                                                                                                                                                                                                                                              IPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLNRVFHDVTHTHV
                                                                                                                                                                                                                                                                                                                                                                     NISGKKYGRFANHFDÞMSÞIFNDRERVÓVLLSDFGLLAVFYAIKLLVAAKGAAWVINMYA
                                                                                                                                                                                                                                                                                                                                                                                                                             YSHRNHHANTNSLDNDEVYIPKRKSKVKIYS--KLLNNPPGRVFTLVFRLTLGFPLYLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FWYHKM 377
                                                                                                                                                                                                                                                                                              APVVGLNAFIIMITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHV
                                                                                                                                                                                                                                                                                                                                                       NISGKKYQRFANHFDPLSPIFSERERIQVVLSDVGLIAVFYGLKFLVAKKGFGWVMRMYG
                                                                                                                                                                                                                                                                                                                                                                                                              YSHRKHHANTNSLENEEVYIPKAKSQLRNYSNFKFLDNTPGRIFILLIMLTLGFPLYLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLPYLAWPVYWFCQSSILTGLWVIGHECGHHAYSEYQWVDNTVGFILHSFLLTPYFSWK 138
                                                                                                                                                                            WXHXWY
                                                                                                                                                                                                                                      LHHLFPYIPHYHAKEASDAIKPVLGEYRMIDRTPFYKAMWREAKECIYIEPDEDKKHKGV
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                                                                                                     383
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Pred. No. 1.2e-152;
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Borago officinalis fatty acid hydroxylase enzyme

31-MAY-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to nucleic acid fragments encoding plant fatty acid modifying enzymes associated with conjugated double bond formation, comprising a modification of delta-9 position or a delta-12 position of fatty acids. The nucleic acid fragments are useful for creating chimeric gene which is useful for creating transgenic plants having altered lipid profiles. They are also useful for producing seed oil containing fatty acids comprising a modification at delta-9 position or delta-12 position. The seed is useful for improving the carcass quality of an animal by supplementing a diet of the animal with animal feed. The nucleic acid fragments encoding homologous fatty acid modified enzymes from the same or other plant species. The present sequence is Borago officinalis fatty acid hydroxlase enzyme. It is a fatty acid modifying enzyme associated with conjugated double bond formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid fragment encoding plant fatty acid modifying enzyme associated with modification of delta-9 position of the fatty acid, useful for creating transgenic plants having altered lipid profiles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borage; fatty acid hydroxylase; conjugated double bond; delta-9; delta-12; transgenic plant; seed oil.
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361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                             LLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRD 295
                                                                                                                                                                                             TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK 235
                                                                                                                                                                                                                                                               TVGLLLHSALLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKRSGISWSSEYLNNPPGRVL
                                                                                                                                                                                                                                                                               | IVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVF 175
                                                                                                                                                                                                                                                                                                                               VIAALFFYTASRYIHLQPHPLSYVAWPLYWFCQGSVLTGVWVIAHECGHHAFSDYQWLDD
                                                                                                                                                                                                                                                                                                                                                                                                                     MGAGGRMSDPSEGK----NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
                        ECIYIEPDEDSEHKGVFWY 374
                                                            YGFLNKVLHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGDYYQCDRTFVFKAMYREVK 360
                                                                                                                                                                                                                                                                                                                                                IVAYVEYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDD
                                                                               FGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK 355
                                                                                                                              RLVAAKGVAWVVCYYGVPLLVVNGFLVLITYLQHTQPSLPHYDSSEWDWLKGALATVDRD
                                                                                                                                                                                                                                                                                                                                                                                                MGGGGRMPVPTKGKKSKSDVFQRVPSEKPPFTVGDLKKVIPPHCFQRSVLHSFSYVVYDL
ECIYVEADEGDNKKGVFWY 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.2%; Score 1396.5; DB 4 63.9%; Pred. No. 5.4e-134; tive 62; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Best Local
                                                                                                                                                                                                                                                                                                The invention relates to a method for modifying the endogenous oil of a cotton plant, to produce cotton seed oil. The method comprises producing a transgenic cotton plant having a gene construct which includes a fatty acid biosynthesis gene operably linked to a promoter sequence capable of conferring expression of the delta9-desaturase (delta9 stearcyl-ACP desaturase) gene, or fatty acid delta12-desaturase (olevyl-PC delta12-desaturase) gene in the seed of a cotton plant. The invention is useful for producing cottonseed oil with reduced palmitic and/or linoleic acid content, and increased stearic and/or oleic acid content. The present sequence is cotton oleoyl-PC delta12-desaturase (ghPAD2-2) protein related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying endogenous oil of cotton plants, to produce cotton seed oil with reduced palmitic and/or linoleic acid content, involves producing transgenic plants containing a fatty acid biosynthesis gene in a
                                                                                                                                                                                                                                                                         Sequence 383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD22380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid; linoleic acid; stearic acid; oleic acid; transgenic plant; cotton seed oil; oleoyl-PC delta12-desaturase; FAD2-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2002
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                                                                                                                                                                                                                 Local Similarity
nes 230; Conserv
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                                                                                                                                                        TVGLILHSSLLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKKSGLRWMAKHFNNPPGRFL
                                                       IVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLANPPGRVF 175
TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK 235
                                                                                                 IVAYVFYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Singh S,
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; 201pp; English.
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                                                                                                                                                                                                                              65.1%;
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                                                                                                                                                                                                            70;
                                                                                                                                                                                                                 Score 1332.5; DB 4;
Pred. No. 1.9e-127;
70; Mismatches 74;
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G
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                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                            Length 383;
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                    This invention describes a novel nucleic acid encoding a polypeptide with desaturase activity. The products of the invention are used in the construction of constructs, vectors, organisms and transgenic plants containing the desaturase. The invention also describes methods for preparing oils or triglycerides with increased content of unsaturated fatty acids; oils, fats and fatty acid mixtures and a novel nucleic acid encoding a protein able to convert a fatty acid to a more highly unsaturated acid. The products of the invention are used to produce transgenic plants (or other organisms) that produce oils and fats with increased contents of unsaturated fatty acids, useful in preparation of foods, animal feeds, cosmetics and pharmaceuticals and in homology screening for isolation of genomic sequences. This sequence represents the bunica granatum (pomegranate) delta-12-desaturase PUFADI2 described
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid encoding desaturase enzymes from pomegranate, useful for recombinant production of unsaturated fatty acids, for e.g. the production of food, animal feeds and pharmaceuticals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               food; animal feed; cosmetic; pharmaceutical;
delta-12-desaturase; PuFADI2; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2004
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disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE40488
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ID AAE13
XX AAE13
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Best Local
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Pred. No. 2.5e-127;
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RESULT 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for modifying the endogenous oil of a cotton plant, to produce cotton seed oil. The method comprises producing a transgenic cotton plant having a gene construct which includes a fatty acid biosynthesis gene operably linked to a promoter sequence capable of conferring expression of the delta9-desaturase (delta9 stearoyl-ACP desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-desaturase) gene in the seed of a cotton plant. The invention is useful for producing cottonseed oil with reduced palmitic and/or lincleic acid content, and increased stearic and/or oleic acid content. The present sequence is soybean microsomal omega-6 desaturase, gmFAD2-2 protein
                                                                Calendula officinalis
                                                                                                pharmaceutical;
                                                                                                              CoFad2; linoleic acid; conjugated fatty acid; plant; cosmetic;
                                                                                                                                                                                  08-MAR-2002
                                                                                                                                                                                                                                                 AAG80695 standard; protein; 383
                                 WO200185968-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related to the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying endogenous oil of cotton plants, to produce cotton seed oil with reduced palmitic and/or linoleic acid content, involves producing transgenic plants containing a fatty acid biosynthesis gene in a
                                                                                                                                               officinalis CoFad2 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                FGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGAGGRMSDPSEGK----NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVAYVFYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLAMAKGLAWVVCVYGVPLLVVNGFLVLITFLQHTHPALPHYTSSEWDWLRGALATVDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK 235
                                                                                                                                                                                                                                                                                                                                   ECIYVEPDQSTESKGVFWYN
                                                                                                                                                                                                                                                                                                                                                                    ECIYIEPDEDSEHKGVFWYH 375
                                                                                                                                                                                                                                                                                                                                                                                                    YGILNKVFHNITDTHVAHHLFSTMPHYHAMBATKAIKPILGBYYRFDBTPFVKAMWRBAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVGLILHSALLVPYFSWKYSHRRHHSNTGSLERDEVFVPKQKSCIKWYSKYLNNPPGRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLAVTLTLGWPLYLALNVSGRPYDRFACHYDPYGPIYSDRERLQIYISDAGVLAVVYGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGAGGRTDVPPANRKSEVDPLKRVPFEKPQFSLSQIKKAIPPHCFQRSVLRSFSYVVYDL
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                                                                                                 lubricant
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Pred. No. 1e-126;
62; Mismatches 8
                                                                                                                                                                                                                                                                                                                                     380
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RESULT 11
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AC AAW86
XX
DT 04-M2
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standard;

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AAW86153 st; AAW86153; 04-MAR-1999

(first entry)

Protein sequence of F form of wild-type Fad2 gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel polypeptide, CoFac2, capable of catalysing the formation of two conjugated double bonds. The products of the invention can be used for the large scale production of conjugated linoleic acids. The composition may be used for cosmetic or pharmaceutical purposes. The conjugated linoleic acids may be used for coating, painting or cold weather ester-type lubricant purposes. There is coating, painting or cold weather ester-type lubricant purposes. There is not a natural source which is rich in conjugated linoleic acids and chemical processes result in a mixture of several isomers. Plant biotechnology is cost-effective and renewable with little side effects. This sequence represents the Calendula officinalis CoFad2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids which encode a conjugase and its related enzyme a delta desaturase to be used for the large scale production of conjugated linoleic acid and linolenic acid in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                            1 MGAGGRMSDPSEGKNILERVPVD------PFTTLSDLKKAIPTHCFERSVIRSSYYVVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                   BIORIGINAL
KECIYVDKDEEVK-DGVYWY 379
                                                                           DFGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREA 354
                                                                                                                                                                             LTLLVTLTLGWPLYLTENVSGRYYDRFACHFDPNSPIYSKRERAQIFISDAGILAVVFVL
                                                                                                                                                                                                                                        DTVGLVLHSFLLVPYFSWKYSHRRHHSNTGSIEHDEVFVPXLKSGVRSTARYLNNPPGRI
                                                                                                                                                                                                                                                          DIVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRV 174
                                                                                                                                                                                                         FTLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAI 234
                                                                                                                                                                                                                                                                                                                                                           MGAGGRMQDPTNGGNKTEPEPIQRVPHEKPPFTVGDIKKAIPPHCFNRSVIRSFSYVFYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 1; 49pp;
                             KECIYIEPDEDSEHKGVFWY 374
                                                           DYGILNKVFHNITDTHVAHHLFSTMPHYHAMBATKVIKPILGDYYQFDGTSIFKAMYRET
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                                                                                                                                                                                                                                                                                                                                                                                                                      57; Mismatches
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Pred. No. 1.6e-126;
7; Mismatches 83;
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Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Brassica plants containing recombinant nucleic acid constructs comprising (a) a wild-type microsomal Delta-12 fatty acid desaturase (Fad2) coding sequence linked to a regulatory sequence and (b a wild-type microsomal Delta-15 fatty acid desaturase (Fad3) coding sequence linked to a regulatory sequence. The plants exhibit a seed-specific reduction in native Fad2 and Fad3 gene expression. The plant produces seeds yielding an oil whose fatty acids comprise at least 86 percent oleic acid and less than 2 percent erucic acid. The plants are used to produce cannola (rapeseed) oil having a high oleic acid content, low erucic acid content, a low alpha-linolenic acid content and high oxidative stability. The present sequence represents the protein sequence of the F form of the wild-type Fad2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica; recombinant; microsomal; delta-12 fatty acid desaturase; oil; delta-15 fatty acid desaturase; seed; fatty acid; oleic acid; Fad3; erucic acid; canola; rapeseed; linolenic acid; oxidative; Fad2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 17-20; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic brassica plants containing delta-12 and delta-15 desaturase constructs - used for producing oil with high oleic acid and low erucions
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                                                                                                                                                                                                     TLVFRLTLGFPLYLLTNISGKKY-GRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAI
                                                                                                                                                                                                                                              TVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKKSDIKWYGKYLNNPLGRTV
                                                                                                                                                                                                                                                                                                                                                                                               MGAGGRM--SDPSEGK--NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
KECIYIEPDEDSEHKGVFWYH
                                                  DYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPVVKAMWREA
                                                                   DFGFLNRVFHDVTHTHVLHHLISYIFHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREA
                                                                                                               FRYAAAQGVASMVCFYGVPLLIVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDR
                                                                                                                                  KLLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDR
                                                                                                                                                                               MLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYGL
                                                                                                                                                                                                                                                                            IVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVF 175
                                                                                                                                                                                                                                                                                                         MGAGGRMQVSPPSKKSETDTIKRVPCETPPFTVGELKKAIPPHCFKRSIPRSFSYLIWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 5.9e-126;
1; Mismatches 81;
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Best Local S
Matches 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to fatty acid desaturases (FAD) from Brassicaceae or Helianthus, where the FAD genes comprise at least one mutation in their sequences. The mutation is in a region encoding the His-Xaa-Xaa-Xaa-His motif of the delta-12 or delta-15 fatty acid desaturases. The invention also provides methods for producing the FAD mutant genes and gene products. The products can be used for producing plants and seeds which have altered fatty acid compositions, e.g. an elevated oleic acid content, a decreased, stabilised limoleic acid content, both elevated oleic acid and decreased, stabilised limoleic acid content or a decreased, stabilised limoleic acid content or a decreased, stabilised limoleic acid and increased level of limoleic acid. The plants may be e.g. soybean, rapsesed, sunflower, safflower, castor bean or corn. The present sequence represents the amino acid sequence of the Brassica wild-type Fad2-F gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated mutant fatty acid desaturase
Brassicaceae or Helianthus plants, used for
having altered fatty acid compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 73-75; 116pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 233; Conser
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                                                                                                                                                                                                                                                                                                                                                                             1 MGAGGRM--SDPSEGK--NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
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                                                                                           TVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKKSDIKWYGKYLNNPLGRTV
                                                                                                                          IVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVF 175
                                                                                                                                                                                                                                                  IVAYVFYYLANTYIPLIPTPLAYLAMPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDD
                                                                                                                                                                                                                   IIASCFYYVATTYFPLLPHPLSYFAWPLYWACQGCVLTGVWVIAHECGHHAFSDYQWLDD
                                                                                                                                                                                                                                                                                                                                       MGAGGRMQVSPPSKKSETDTIKRVPCETPPFTVGELKKAIPPHCFKRSIPRSFSYLIWDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00874109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roh
Loh
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1318; DB 2;
Pred. No. 5.9e-126;
1; Mismatches 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              se genes - obtained by mutation of for producing plants or seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product.
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                                 The patent discloses Brassica plants and seeds having a long chain monounsaturated fatty acid (FA) content of at least 82% and an erucic acid content of at least 15% based on total FA composition. The patent further relates to genes encoding delta-12 and delta-15 fatty acid desaturases (Fad2 and Fad3 respectively). Mutations in these genes result in useful alterations in the fatty acid compositions of the seed oil e.g. mutation in Fad2 gene confers elevated oleic acid content and decreased linoleic acid content. The Brassica seeds are useful source for vegetable oil and industrial oils such as engine lubricants, transmission fluids for diesel engines and hydraulic oil. The present sequence is that of Brassica napus microsomal wild type delta-12 fatty acid desaturase-F (n-2-2-5)
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Long chain monounsaturated fatty acid; erucic acid; oleic acid; delta-15 fatty acid desaturase; Fad3; linoleic acid; vegetable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200007433-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70114 standard; protein; 384
                                                                                                                                                                                                                                                                                                                                                      (CRGI ) CARGILL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta-15 fatty acid desaturase; Fad3; linoleic acid; vegetable oil;
industrial oil; lubricant; hydraulic oil; delta-12 fatty acid desaturase;
Fad2; Fad2-F; rapeseed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70114;
                                                                                                                                                                                                                                         Brassica plants and
ty acid content, for
                                                                                                                                                                                                                                                                                               2000-223937/19
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  384
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                                                                                                                                                                                                                                       content,
                                                                                                                                                                                                            Page 104-105; 117pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                98US-00128602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                      seeds having elevated long chain monounsaturated
industrial uses, e.g. engine lubricants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conserved_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delta-12 fatty acid desaturase-F
                                                                                                                                                                                                                                                                                                                          둤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fad2-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
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Query Match Best Local Similarity

64.4%;

Score Pred.

1318; DB 3; No. 5.9e-126;

Length 384;

in plant seeds and comprises transforming a plant with a nucleic acid construct (I) comprising a seed-specific regulatory sequence linked to either a mutant delta-12 or delta-15 fatty acid desaturase (FAD) gene encoding a protein with a mutation in a His-(Asp/Glu)-Cys (Gly/Ala)-His amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15

The invention relates to a method for altering the fatty acid composition

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                                                                                  Altering fatty acid profiles nutritional value of seeds.
                                                                                                              N-PSDB;
                                                                                                                                          Broglie RM,
                                                                                                                                                                              26-MAR-1998;
                                                                                                                                                                                                                                                                                                                                15-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                     AAY27329
                                                                 Example;
                                                                                                                                                                                                26-MAR-1998;
                                                                                                                                                                                                                 29-SEP-1999
                                                                                                                                                                                                                                    EP945514-A1.
                                                                                                                                                                                                                                                      Brassica napus
                                                                                                                                                                                                                                                                        genetic
                                                                                                                                                                                                                                                                                  Fatty acid;
linoleic aci
                                                                                                                                                                                                                                                                                                                                                   AAY27329
                                                                                                                                                           (DUPO)
                                                                                                                                                                                                                                                                                                             napus delta-12
                                                                                                               1999-530050/45.
DB; AAX91076.
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                                                                                                                                                           먾
                                                                                                                                                                                                                                                                       mapping;
                                                                                                                                                                                                                                                                                id; delta-12 desaturase; fatty acid desaturase;
acid; alpha-linolenic acid; mutant; nutritional
                                                               Page 19-21; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKKSDIKWYGKYLNNPLGRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPVVKAMWREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLVFRLTLGFPLYLLTNISGKKY-GRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAI 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRYAAAQGVASMVCFYGVPLLIVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDR
                                                                                                                                                                                                                                                                                                                                                                                                                 KECIYVEPDRQGEKKGVFWYN
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                                                                                                                                                           PONT DE NEMOURS & CO
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                                                                                                                                         Miao G,
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                               98EP-00302322
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                                                                                                                                                                                                                                                                        plant
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                                                                                                                                          Debonte LR,
                                                                                                                                                                                                                                                                        breeding.
                                                                                                                                                                                                                                                                                                             acid
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                                                                                                                                                                                                                                                                                mutant; nutritional
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                                                                                                                                          RS,
                                                                                                                                                                                                                                                                                                             (FAD2)
                                                                                            useful
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                                                                                                                                                                                                                                                                                            FAD;
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                                                                                                                                                                                                                                                                                          enzyme;
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ID ABBRO028
AC ABBRO
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XX ABBRO
XX ABRO
DT 26-JU
XX Rape
CX Rape
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XW delt;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC FAD. Expression of this construct in plants decreases the level of CC activity of these enzymes in the cells of the plant i.e. the construct comprising a mutant delta-12 cc gene is used to decrease the level of linoleic acid in the seeds of CC plants to (soybean, rapeseed, sunflower, cil palm, coconut palm, flax, CC castor and peanut) Similarly a construct comprising a mutant delta-15 cc gene is used to decrease the levels of alpha-linolenic acid in the seeds of plants, especially Brassica canola. The new method may also be used to transform a plant with both (1) comprising DNA encoding mutant delta-12 cc and (1) comprising DNA encoding mutant delta-12 cc the levels of both linoleic and alpha-linolenic acid simultaneously in comprise seeds. These methods alter the nutritional value of the seeds of clasmostic markers in plant genetic mapping and plant breeding programs. Cc In addition (1) may been transformed. (1) may also be used as DNA cc diagnostic markers in plant genetic mapping and plant breeding programs. Cc maddition (1) may been to isolate other related FAD genes. The cc present sequence represents a Brassica napus wild type D form of cc microsomal delta-12 fatty acid desaturase 2 (FAD2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                Rape; microsomal delta-12 desaturase; delta-12 hydroxylase; delta-12 fatty acid hydroxylase; enzyme; plant; vegetable o fat; oil; heart disease.
                    16-APR-2002
                                                          US6372965-B1
                                                                                          Brassica napus
                                                                                                                                                                                                            Rape microsomal delta-12 desaturase amino acid sequence
                                                                                                                                                                                                                                                                                                                              ABB80028 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGAGGRM-----SDPSEGKNILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Mismatches
                                                                                                                                                    vegetable oil; seed oil;
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AKECIYIBPDEDSEHKGVFWYH

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RDYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPVVKAMWRE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid fragment encoding or CC comprising a sequence encoding a plant enzyme that is a delta-12 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase. CC Chimeric genes comprising nucleic acids of the invention are used to CC create transgenic plants with altered levels of unsaturated fatty acids, CC and can modify plant lipid composition. Nucleic acids of the invention CC can be used as hybridisation probes to isolate or amplify nucleotide CC sequences encoding other fatty acid desaturases or fatty acid desaturase-CC related enzymes. They can also be used in restriction fragment length CC polymorphism (RPLP) breeding to obtain altered levels of oleic acids in CC seed oil of oil producing plant species. They can also be used to produce CC seed oil containing altered levels of unsaturated fatty acids. Nuclecic acids of the invention can combine the high oleate trait of transformed CC seed with mutations for altered fatty acid compositions to obtain new fatty acid compositions and/or improved agronomy. A vegetable oil low in CC total saturates and high in monounsaturates would provide significant CC health benefits to consumers (reduced risk of coronary heart disease) as well as economic benefits to oil processors. The current sequence CC represents a rape microsomal delta-12 desaturase amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Yadav NS;
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15-OCT-1993;
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RDFGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYRE
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                                                      LYRYAAVQGVASMVCFYGVPLLIVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVD
                                                                                                                                  VMLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYG
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8; Mismatches 82;
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Search completed: June 18, 2004, 17:36:25 Job time: 61 secs

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-MODBLETRAMBE PARAMETER - START=1 - SUPFIX=rge -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
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-DCCALIGN=15 -MODE=LOCAL
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-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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37: em htg_mam:*
38: em htg_mam:*
40: em htgo_hum:*
41: em htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

ŏ 1336 1335 1332.5 1325.5 1323.5 1323.5 1323.5 1318 1318 1318 1318 1318 1318 1359.5 1350.5 1350.5 1348.5 1347.5 1339.5 1337.5 1337.5 1360 1359.5 1366. 1589. 1578. 1541. 1396. 1387. 1374. 1366. 1592. 1592. 1592. 589 589 Score 100.0 100.0 93.9 80.3 79.6 Match Length DB AY166773 AY166776 CAY166776 CAY166778 AY166777 AX367438 AX031162 BD061164 CPY16283 AX031160 BD061164 CPY16283 AX0462108 AF074324 AF525534 ARF251843 ARF251843 AF251844 AF251844 AF251844 AF251844 AF251844 AF251846 AF718477 AF34306377 PGR437139 AX700111 PCU86072 AB094415 AF7331163 CCYMO6DA AX301157 AF3331163 AX0574065514 BD2613614 COF245938 AX089471 AR367438 Sequence AX031162 Sequence BD061165 Plant fat AR367437 Sequence AX031160 Sequence BD061164 Plant fat U86072 Petroselinu AB094415 Spinacia AF331163 Gossypium Y16284 Crepis pala Y10112 Gossypium h L43921 Glycine max X92847 S.commerson AY178447 Punica gr AP006377 Lotus cor AJ437139 Punica gr AX700111 Sequence Y16283 Crepis pala AR064128 Sequence AY462108 Stokesia AF074324 Borago of AF525534 Vernicia AR066514 BD261361 AR184297 AR431239 BD132762 AR184295 AF188264 AF251844 AF188263 AF192486 AJ292275 AF251843 AY057406 AX301157 Sequence AF343065 Calendula AY083163 Olea euro AJ245938 Calendula AX089471 Sequence Description AY166776 Rudbeckia AY166773 Helianthu 5 Crepis alpi 778 Helichrys 777 Dimorphot 4 Vernonia 4 Helianthu 3 Vernonia Sequence Sequence Sequence Fatty aci Sesamum i Helianthu Persea am Helianthu

ALIGNMENTS

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ION Calendula officinalis partial management (des8.11 gene).

ION AJ245938

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Ocalendula officinalis

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calendula.

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Submitted (02-SEP-1999) Feussner I., Hormonforschung,
Pflanzenbiochemie, Weinberg 3, D-06120 Halle/Saale, G
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                                                                                        MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLy8AsnIleLeuGluArgVal
GluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAlaTyrVal
                                                 ProValAspProProPheThrLeuSerAspLeuLysLysAlaIleProThrHisCysPhe
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/protein_id="CAB64256.1"
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KIYSKLLNNPPGRVFTLVFRTLTGFPFLYLLTNISGKKYGRFANHFDPMSPITNDERRV
VIYSKLLNNPPGRVFTLVFTLTLGFPFLYLLTNISGKYGRFANHFDPMSPITNLHTHLSLPH
YDSTEMMYIKCALSTIDRDFGFLNRVFHDVTHTHVLHHLISYIPHHAKEARDAIKEV
LGEYYKIDRTPIFKAMYREAKECIYIBPDEDSEHKGVFWYHKM"
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/db_xref="taxon:41496"
/clone="pCoDes8.11"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Calenduleae; Calendula.
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                                              CTCCATTCGGCTCTCACCCCGTATTTCTCTTGGAAATATAGCCACAGGAATCACCAC
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GCCAACACAAATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTC
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y acid desaturase gene from plants
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AKTIENGESELLSCHAFT (DE)
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KIYSKLLNNPPGRVFTLVFRLTLGFPLYLLTNISGKKYGFFANHFDRWS JFNDRERV
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                                          Direct Submission
Submitted (18-OCT-2002) Crop Gene
Experimental Station, Wilmington,
                                                                                Cahoon, E.B.
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          organism="Helianthus"
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1 (bases 1 to 1419)
Cahoon, E.B., Schmurr, J.A., Huffman, E.A. and Minto, R.E.
Cahoon, B.B., Schmurr, J.A., Huffman, E.A. and Minto, R.E.
Fungal responsive fatty acid acetylenases occur widely
evolutionarily distant plant families
plant J. 34 (5), 671-683 (2003)
2 (bases 1 to 1419)
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'mol_type="mRNA"
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GHHAYSDYQLIDDIVGFVHSALYTPYESWKYSHRNHHANTNSLDDLBVFFFERKRIV
AVYSKLIANPPGRVFTLYFRLTGFFLYTLTVLSGKKYGFFANHFDDLSPIFTERERI
QVVISDIGILAVLYATKLLVEAKGAAWVTCMYLIPULGVHMFFVLITYLHHTHLSLPH
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                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                    organism="Rudbeckia
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Cahoon,E.B.
Direct Submission
Submitted (19-CCT-2002) Crop Genetics, DuPont, Bl
Experimental Station, Wilmington, DE 19880-0402,
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Cahoon, E.B., Schnurr, J.A., Huffman, E.A. ar Fungal responsive fatty acid acetylenases evolutionarily distant plant families plant J. 34 (5), 671-683 (2003)
2 (bases 1 to 979)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Rudbeckia.
1 (bases 1 to 979)
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lipvmgyhmffylhtthlslphydstemnwikgalstidrdefelarvfhdvth
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                                                                                                                                             AspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeu
GluAlaLysGluCysIle
                                     ProValLeuGlyGluTyrTyrLy8IleAspArgThrProIlePheLy8AlaMetTyrArg
                                                                          CATCATTTGATCTCATACATCCCACATTATCATGCAAAGGAGGCAAGGGACGCAATCAAG
                                                                                                                                                                                            SerLeuProHisTyrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-JAN-1998) M.A. Lee, Nilsson Webull Ab, S-26881, Svalov, SWEDEN Revised by [4]
3 (Dases 1 to 1435)
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Nilsson, R., Liljenberg, C.,
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/db xref="taxon:72610"
/clone="pCREP1"
/clone_lib="lambda ZAP"
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/translation="MGGGGGGTGTKOKTHENDEFTVSDLKQAIPPHCFKRSVIR
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HAFSDYQWVDDTVGFILHSFLMTPYFSWKYSHRNHHANTNSLDNDEVYIPKSKAKVAL
YYKVLMHPPGHLLIWFITFTLGFFLYLFTNISGKKYERFANHFDDMSDIFKERERFQV
LLSDLGLLAVLYGYKLAVAAKGAAWTCIVGIPVLGVFIFDIITYLHTHLSLLFVD
SSEWNWLRGALSTIDRDFGFLNSVLHDVTHTHVMHHLFSYIPHYHAKBARDAINTVLG
                                                                                                                                                                                             DFYKIDRTPILKAMWREAKECIFIEPEKGRGSKGVYWYNKF"
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NVSGKKYERFANHFDDLSFIFTERERIQVVLSDLGIIAVFYAVRLLVAAKGLSWVLSM

YVIPVLGVHAFFVLITYLHHTHLSLPHYDSTEWKWIKGALSTIDRDFGFLNRVFHDVT

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Cahoon,E.B., Schnurr,J.A., Huffman,E.A. and Minto,R.E.
Fungal responsive fatty acid acetylenases occur widely
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   Cahoon, E.B.
Direct Submission
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                                                                 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe
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Green,A., Singh,S., Lenman,M. and Stymne,S.
Plant fatty acid epoxygenase genes and uses therefor
Patent: US 6329518-A 3 11-DEC-2001;
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  AlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly
                                    ValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeu
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterida; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Crepis.
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Plant fatty acid epoxygenase genes and uses therefor Patent: WO 9846762-A 3 22-OCT-1998;

GREEN ALLAN (AU); SINGH SURINDER (AU); COMMW SCIEN (AU); STYMNE STEN (SE); LENMAN MARIT (SE)
ArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysLysTyrGly 199
                                                                                             ValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPhe
                                                                                                                                                                                       HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLysSerLys
                                                                                                                                                                                                                                                                                                                                                                       HisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAspIleValGlyPhe
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                                                                                                                                                                                                                                                                           ValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSerHisArgAsnHis
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                                                                    CTCAAGCGTATCTATAAACTTCTTAACAACCCACCTGGTCGACTGTTGGTTTTTGGTTATC
                                                                                                                                                         CATTCCAACACAAGTTCGATTGATAACGATGAAGTTTACATTCCGAAAAGCAAGTCCAAA
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/db_xref="GI:10278516"
/db_xref="GI:10278516"
/db_xref="REMTREMEL:CAC09645"
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RSSYYVVQDLIIAYIFYFLANTYIPNLPHPLAYLAWPLYWFCQASVLTGLWILGHECG
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RIYKLLNNPGRELLVLUMFTLGFBLYLLTUNISGKKYLDFANHFDPMSFIFTEREREFQ
VFLSDLGLLAVFYGIKVAVANKGAAWVACMYGVPVLGVFTFFDVITFLHHTHQSSPHY
DSTEMMWIRGALSAINXDFGFLMSVFHDVTHHVMHHLFSYIPHYHAKEARDAIKPIL
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/mol_type="unassigned DNA"
/db_xref="taxon:137775"
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                                                                                  Stymne, S., Green, A., Singh, S. and Lenman, M.

plant fatty acid epoxygenase genes and uses the:

Patent: JP 2001518797-A 2 16-OCT-2001;

COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
STYMNE

OS Crepis sp.
PN JP 2001518797-A/2
PN JP 2001518797-A/2
PP 16-OCT-2001
PF 09-APR-1998 JP 1998543302
PR 15-APR-1997 AU PO 6223,15-APR-1997 AU
16-APR-1997 US 60/043706,20-JUN-1997 US 60/043706,20-JUN-199
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/organism="Crepis sp."
/mol_type="genomic DNA"
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          ACTGAATGGAACTGGATCAGAGGGGGCTTTGTCAGCAATCGATAGNGACTTTGGGTTCCTG
                   ThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeu
                                                   PhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeuProHisTyrAspSer
                                                                                     AlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIleProValLeuGlyValSerVal
                                                                                                               GTCTTCCTTTCGGATCTTGGTCTTCTTGCTGTGTTTTATGGAATTAAAGTTGCTGTAGCA
                                                                                                                        AGGTTTGCCAACCACTTCGACCCCATGAGTCCAATTTTCAAAGAACGTGAGCGGTTTCAG
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Green, A., Singh, S., Lenman, M. and S Plant fatty acid epoxygenase genes Patent: US 6329518-A 1 11-DEC-2001;
                                                                                                                                                                          ProValAspPro---ProPheThrLeuSerAspLeuLysLysAlaIleProThrHisCys
                                                                                                                                                                                                          MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal
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ATCGAGCCT-----GATAGCAAGCTCAAAGGTGTTTATTGGTATCATAAATTG
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/mol_type="genomic |
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Green,A., Singh,S., Stymne,S. and Lenman,M. Plant fatty acid epoxygenase genes and uses therefor Patent: WO 9846762-A 1 22-OCT-1998; GREEN ALLAN (AU); SINGH SURINDER (AU); COMMW SCIEN (AU); STYMNE STEN (SE); LENMAN MARIT (SE)
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                              /mol_type="unassigned |
/db_xref="taxon:32644"
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 codon_start=1
               note="unnamed protein product"
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KEYWORDS SOURCE ORGANISM

REFERENCE

AUTHORS TITLE JOURNAL

FEATURES

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US-10-069-772-2 (1-377) x AX031160 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal 6.88e-140 1589.50 85.98% 75.40% 77.65% -----GGTCGGACATCGGAAAAATCGGTCATGGAACGTGTC (1-1358)Mismatches: Indels: Gaps: Length:
Matches:
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CE 1 (bases 1 to 1358)

CE 1 (bases 1 to 1358)

RS Stymne, S., Green, A., Singh, S. and Lenman, M. Plant fatty acid epoxygenase genes and uses therefor Patent: JP 2001518797-A 1 16-OCT-2001;

COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN STYMNE PN JP 2001518797-A/1

PN JP 2001518797-A/1

PN 19-APR-1998 JP 1998543302

PR 15-APR-1998 JP 1998543302

PR 15-APR-1997 AU PO 6223, 15-APR-1997 AU PO 6226 PR 15-APR-1997 US 60/050403 PI STEN STYMNE, ALLAN GREEN, SURINDER SINGH, MARIT LENMAN PC CLINI5/53, CLIN9/02

CC Strandedness: Single; FT Key 30, .1151.
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|TTCCAGAGATCTGTAATCCGCTCATCTTACTAGTTGTTCAAGATCTCATTATTGCCTAC
IleGluProAspGluAspSerGluHisLysGlyValPheTrpTyrHisLysMet 377
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Submitted (21-JAN-1998) M.E. Lenman, Dept of Plant Breeding
Research, SLU, Herman Ehles V 2-4, 26831 Svalov, SWEDEN
Location/Qualifiers
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Nilsson,R.,
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delta 12 fatty acid epoxygenase.
Crepis palaestina
Crepis palaestina
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Science 280 (5365), 915-918 (1998)
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Green,A. and Stymne,S.
Identification of non-fileme diiron proteins that catalyze triple
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                 PheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAlaTyr
                                                         ProValAspPro---ProPheThrLeuSerAspLeuLysLysAlaIleProThrHisCys
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/protein_id="CAA76156.1"
/db_xref="GI:3135018"
/db_xref="GOA:065771"
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|clone="pcpal2"
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                                                                                                                            ATCGAGCCT----
                                                                                                                                            IleGluProAspGluAspSerGluHisLysGlyValPheTrpTyrHisLysMet
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Qy 252	Qy 232 TyrålaileLysLeuLeuValålaAlaLysGlyålaÅlaTrpValileAsnMetTyrA	Qy 212 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe ::::: ::: :::	Qy 192 AsnIleSerGlyLysLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIle	Qy 172 GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThr	Qy 154 ProLysArgLysSerLysValLysIleTyrSerLysLeuLeuAsnAsnProPro	Qy 134 TyrSerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIle	Qy 114 AspAspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLy ::	Qy 94 GlyLeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIle	Qy 74 ThrProLeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThr	Qy 54 AspleuileValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIlePro	Qy 34 AlaIleProThrHisCysPheGluArgSerVallleArgSerSerTyrTyrValValHis	Qy 15 AsnIleLeuGluArgValProValAspProProPheThrLeuSerAspLeuLysLys	US-10-069-772-2 (1-377) x AR064128 (1-1364)	Alignment Scores: Pred. No.: 1578.50 Score: 1578.50 Matches: 280 Percent Similarity: 87.16% Best Local Similarity: 76.50% Mismatches: 44 Query Match: 77.11% Gaps: Caps: Gaps:	AUTHORS Hitz, W.D. AUTHORS Hitz, W.D. Fatty acid modifying enzymes from developing seeds of Vernon. JOURNAL Patent: US 5846784-A 3 08-DEC-1998; FEATURES Location/Qualifiers 11364 /organism="unknown" /mol_type="unassigned DNA"
euHisHisThrHis 271 	leAsnMetTyrAla 251 :: rGCGCATGTACGGA 876	euLeuAlaValPhe 231 ::: CATTGCTGTGTTT 816	roMetSerProIle 211 ::: CGTTGAGCCCCATC 756	euTyrLeuLeuThr 191 ATACCTCTTGACC 696	euAsnAsnProPro 171 ::: TGACAACACCCCT 636	<pre>spGluValTyrile 153 :: aggaggTTTACATT 576</pre>	YrPheSerTrpLys 133 ACTTTTCTTGGAAA 516	<pre>spTyrGlnLeuIle 113 :: </pre>	laSerIleLeuThr 93 :: CTTCGATCCTCACT 396	leProLeuIlePro 73 ::: TCCTCTTCTTCCT 336	yrTyrValValHis 53 GCTACGTTGTTCAG 276	erAspLeuLysLys 33 CGATCTAAAGAAA 216		· .	0 H

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Search completed: June 23, 2004, 16:53:19 Job time: 3312 secs

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ALIGNMENTS

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Rape micr

This invention describes a novel isolated nucleic acid sequence (I) encoding a Calendula officinalis calendulic acid desaturase polypeptide. The invention also describes (I) a process for producing unsaturated fatty acids, comprising introducing at least one copy of (I) or (II) introducing organism, growing the organism, isolating oil from the

into

New nucleic acid sequence encoding Calendula officinalis calendulic acid desaturase, useful for e.g. producing transgenic plants having oil with an increased unsaturated fatty acid content,.

Claim 1b; Page 13-15; 22pp; German.

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CC organism and releasing fatty acids from the oil;(2) a process for CC producing triglycerides with an increased unsaturated fatty acid content, CC comprising introducing at least one copy of (I) or (II) into an oil-CC producing organism, growing the organism and isolating oil from the CC organism; (3) a process for producing saturated fatty acids, comprising CC introducing at least one nonfunctional copy of (I) or (II) into an oil-CC producing organism, growing the organism, isolating oil from the organism (CC and releasing fatty acids from the oil; (4) a process for producing CC triglycerides with an increased saturated fatty acid content, comprising CC introducing at least one nonfunctional copy of (I) or (II) into an oil-CC producing organism, growing the organism and isolating oil from the CC organism; (5) an enzyme capable of converting a diumsaturated fatty acid CC of to a triunsaturated fatty acid. Transgenic organisms (especially containing one or more copies of (I) are useful for producing CC oils with an increased unsaturated fatty acid content. Transgenic CC of (I) are useful for producing Oil with an increased saturated fatty acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for producing CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) and fragments of (I) are also useful for isolating CC acid content. (I) are al
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CCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTGCTATCCGATTTCGGTC
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RESULT 2
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ID AAT9
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OX Crep
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                              29-MAR-1996;
                                                                                     09-OCT-1997.
                                                                                                                                                                                                                     Crepis alpina
                                                                                                                                                                                                                                              Crepis alpina delta 12 acetylenase; plant; yeast; acetylenic compound; farty acid; coating; plastic; lubricant; oilseed; ss.
                                                                                                                                                                                                                                                                                          Crepis alpina delta 12 acetylenase encoding
                                                                                                                                                                                                                                                                                                                      25-MAR-2003
20-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                            AAT95688 standard; DNA; 1128
 (BAFO/) BAFOR
                                                          14-FEB-1997;
                                                                                                                  WO9737033-A1.
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(first ent
                              96SE-00001236
                                                          97WO-SE000247
                                                                                                                                                                           Location/Qualifiers
1. .1128
                                                                                                                                              /product= "Crepis alpina delta 12 acetylenase"
                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                      entry)
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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA encodes the Crepis alpina delta 12 acetylenase. This is used in the production of acetylenic compounds. The process comprises treating C18 fatty acids having a double bond at position delta 12 with an acetylenase to form 12-ynoic acids. The acetylenic compounds can be produced by organisms such as oilseed plants, yeast and fungi which are transformed with this acetylenase DNA. These organisms can accumulate these acetylenic compounds which are chemical feedstocks, particularly for coatings, plasticisers and lubricants. The process enables the production of these acetylenic compounds from a renewable resource with high purity and at reasonable cost. (Updated on 25-MAR-2003 to correct feield.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bafor M,
Sjoedahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1128 BP; 270 A; 308 C; 237 G; 313 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-503117/46.
P-PSDB; AAW36793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 21; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LENM/)
(SJOE/)
(STYM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GUMM/)
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      484
                                                                                    424
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DAHLQVIST A.

GUMMESON P.

LEE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                           TCCAAACTTCTTAACAATCCACCCGGGCGAGTGTTCACTTTGGTGTTTCGGTTGACTTTA
                                                                                                                                                                                          GCTCTCCTCACCCCGTATTTCTCTTTGGAAATATATAGCCACAGGAATCACCACGCCAACACAC
                                                                                                                                                                                                                                                CACCATGCCTTCAGCGACTACCAGTGGGTTGACGACACTGTGGGCTTCATCCTCCACTCG
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                                                                                                                                                                   TTTCTCATGACCCCGTATTTCTCCTGGAAATACAGCCACCGGAACCACCATGCCAACACA
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                                                                                  AATTCGCTTGACAACGATGAAGTTTACATCCCCAAAAGCAAGGCCAAAGTCGCGCTTTAC
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S, Stymne
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S;
    CAACCACCCACCTGGCCGACTGTTGATTATGTTCATCACCCTTCACCCTA
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77.4%;
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Pred. No. 4.7e-167;
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of acetylenic fatty acids
and lubricants.
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97AU-00006223. 97AU-00006226. 97US-0043706P. 97US-0050403P.

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Fatty acid epoxygenase; Cpal2 gene; mixed function delta-12-epoxygenase; epoxygenated fatty acid; tranvegetable oil; oilseed; ss.
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                                                                                                                                                                                                                                                                                   Fatty acid epoxygenase; CrepX; delta-12-epoxygenase; mixed function monooxygenase; epoxygenated fatty acid; transgenic vegetable oil; oilseed; ss
                           09-APR-1998;
                                                                                                                                                                                                                                             Crepis
                                                                                                                                                                                                                                                                                                                                                                           Crepis sp. delta-12-epoxygenase cDNA clone CrepX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This cDNA clone, designated Crepx, codes for a novel epoxygenase (see CC AAW79743) of a Crepis sp. (not Crepis palaestina) that has a high CC vernolic acid content. The Crepx gene shows a high degree of homology to the novel Cpal2 delta-12-epoxygenase gene (see AAW3101) of C. CC palaestina. Crepx cDNA was isolated from a Crepis sp. cDNA library using CC a Crepis alpina acetylenase partial gene sequence (see AAV63104) as probe. The invention relates generally to novel genetic sequences (see CC AAV63101-03) encoding fatty acid epoxygenases (see AAW79742-44), CC especially delta-12-epoxygenases or mixed function monooxygenases. These CC provide the means by which fatty acid metabolism can be manipulated in CC e.g. yeast, mould, bacteria, insecte, birds, mammals and plants CC (especially oilseed plants such as flax), in particular to convert CC unsaturated fatty acids to epoxygenated fatty acids. The invention cexends to genetically modified oil-accumulating organisms and to the CC oils derived from them. These oils can be used in production of coatings, CX resins, glues, plastics, surfactants or lubricants
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15-APR-1997;
16-APR-1997;
20-JUN-1997;
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P-PSDB; AAW79743.
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                                                                                          TTGGAAATACAGTCACCGGAATCACCATTCCAACACAAGTTCGATTGATAACGATGAAGT
                                                                                                                                                                                  TATTCCTACACCTCTGGCTTACCTAGCATGGCCCCGTTTACTGGTTTTGTCAAGCTAGCAT
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    TTACATTCCGAAAAGCAAGTCCAAACTCAAGCGTATCTAAAACTTCTTAACAACCCACC
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10-FEB-1999
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                                                                                                                                                                                                                                                                                                                                     galamenensis; fatty acid desaturase; epoxidising enzyme
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                                                                                                                                                                                                                                                                      galamensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAGAGGGCAGGGAATGCATGTACATCGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGCATCATTTGTTTTCATACATTCCACACTATCATGCAAAGGAAGCAAGGGATGCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
    97US-00872302
                                              97US-00872302
                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding Vernonia galamenensis fatty acid desaturase and fatty epoxidising enzyme - used to alter levels of expression of the enzy transformed host cells or to produce recombinant enzymes.
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P-PSDB; AAW83354.
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                        TATCGGATGTGGGTCTCATTGCTGTGTTTTACGGGCTTAAGTTTCTTGTAGCGAAAAAAG
                                                                                                                      CCAACCACTTTGATCCGTTGAGCCCCATCTTCAGTGAGCGTGAACGAATCCAGGTCGTGC
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17-NOV-1992;
15-OCT-1993;
20-JUN-1994;
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Lightner JE,
Yadav NS;
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CC The invention relates to an isolated nucleic acid fragment encoding or CC comprising a sequence encoding a plant enzyme that is a delta-12 (desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase. CC Chimeric genes comprising nucleic acids of the invention are used to create transgenic plants with altered levels of unsaturated fatty acids, CC and can modify plant lipid composition. Nucleic acids of the invention CC can be used as hybridisation probes to isolate or amplify nucleotide composition entered levels of letty acid desaturase. They can also be used in restriction fragment length CC polymorphism (RFUP) breeding to obtain altered levels of oleic acids in ced oil of oil producing plant species. They can also be used to produce composition can combine the high oleate trait of transformed cc seed oil containing altered levels of unsaturated fatty acids. Nucleic cacids of the invention can combine the high oleate trait of transformed cc seeds with mutations for altered fatty acid compositions to obtain new fatty acid compositions and/or improved agronomy. A vegetable oil low in cotal saturates and high in monounsaturates would provide significant health benefits to consumers (reduced risk of coronary heart disease) as well as economic benefits to oil processors. The current sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Pred. No. 3.4e-102;
0; Mismatches 389;
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                            composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCATTTCTTCCCCAACGCTCCCATCTACAATGACCGAGAACGCCTCCAGATATACCTCT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGATCACATATTTGCACCACACCCATCTCTCACTCCCTCATTATGATTCAACCGAATGGA 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1372 BP;
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ACTGGATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTCCTGAATCGGGTTT
                                                                                   TGATCACATATTTGCACCACACCCATCTCTCACTCCCTCATTATGATTCAACCGAATGGA
                                                                                                                                                     TGGCCTCGATGATCTGCCTCTACGGAGTACCGCTTCTGATAGTGAATGCGTTCCTCGTCT
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Pred. No. 3.4e-102;
0; Mismatches 389;
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desaturase. Substitution of N-terminal OLE1 protein coding sequences with the N-terminal sequence derived from the Arabidopsis FAD2 gene is done to optimise gene expression, membrane targeting and ER (endoplasmic reticulum) retention of the chimeric enzyme. Modified yeast delta-9 desaturase pl-ole1 gene comprising a desaturase domain and a cyt b5 domain, is customised for expression in a plant cytoplasm. This gene is modified for expression in Arabidopsis and related species to obtain transgenic plants that produce a higher yield of unsaturated fatty acids. Transgenic plants, especially oil plants, are produced we because the content of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis FAD2 gene; delta12-desaturase; yeast delta-9 desaturase;
pl-olel_gene; transgenic plant; oil plant; mono-unsaturated fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pl-ole1 gene; transgenic plant;
foodstuff; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 72-73; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression
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produce a higher yield of unsaturated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCACAACATTACAGACACACGTGGCTCATCACCTGTTCTCGACAATGCCGCATTATA
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Query Match 35.5
Best Local Similarity 63.9
Matches 689; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1372 BP; 324
                              ATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTGGGCGAGTACTATAAAATCGACA
                                                                                                                         TCCACGACGTTACACACACTCACGTCTTGCATCATTTGATCTCATACATTCCACACTTATC
                                                                                                                                                                                                               ACTGGATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTCCTGAATCGGGTTTT
                                                                                                                                                                                                                                                                       TGATCACTTACTTGCAGCACACTCATCCCTCGTTGCCTCACTACGATTCATCAGAGTGGG
                                                                                                                                                                                                                                                                                                       TGATCACATATTTGCACCCACACCCATCTCTCACTCCCTCATTATGATTCAACCGAATGGA
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      ACGCAATGGAAGCTACAAAGGCGATAAAGCCAATTCTGGGAGACTATTACCAGTTCGATG
                                                                                                                                                                                     ACTGGCTCAGGGGAGCTTTGGCTACCGTAGACAGAGACTACGGAATCTTGAACAAGGTGT
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Pred. No. 3.4e-102;
0; Mismatches 389;
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Ş Query Match Best Local Sim Matches 689; 109 h 35.5%; Similarity 63.9%; 89; Conservative ATCCACCGTTCACGTTAAGCGATCTGAAGAAAGCGATTCCTACCCATTGCTTTGAGCGAT Score 455.6; DB 3; Pred. No. 3.4e-102; 0; Mismatches 389; Indels 0; Gaps 168

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ACAGGGAAGGTGACAAGAAAGGTGTGTACTGGTACAACAATAAGTTATGAGGATGATG 1320
                                   ATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAAGGTG 1186
                                                                                                                                                 GGACTCCAATTTTCAAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCCG 1128
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                                                                                                  GAACACCGTGGTATGTGGCGATGTATAGGGAGGCAAAGGAGTGTATCTATGTAGAACCGG
                                                                                                                                                                                                          ACGCAATGGAAGCTACAAATGCGATAAAGCCAATTCTGGGAGACTATTACCAGTTCGATG 1202
                                                                                                                                                                                                                                                         ATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTGGGGCGAGTACTATAAAATCGACA 1068
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                                                                                                                                                                                                                                                                                                                              Matches 683;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes Vernonia galamenensis fatty acid desaturase. The present invention also describes: (i) Vernonia galamenensis fatty acid epoxidising enzyme; (ii) chimeric genes comprising the fragments linked to regulatory sequences; and (iii) transformed host cells containing the chimeric genes. The DNA's from the present invention can be used to alter levels of expression of the enzymes in transformed host cells or to produce the recombinant enzymes by transformation of microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                             Sequence 1476 BP; 373 A; 337 C; 346 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding Vernonia galamenensis fatty acid desaturase and fatty acid epoxidising enzyme - used to alter levels of expression of the enzymes transformed host cells or to produce recombinant enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vernonia ga. expression;
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P-PSDB; AAW83353.
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on; chimeric gene; recombinant
GTCACCATGCATTTAGCGACTACCAGTTGATTGATGACATTGTTGGATTCGTGCTCCATT
                                        CTTATTGGGTCGTTCAAGGCTGTGTGCTTACAGGAGTGTGGGTCATAGCCCCATGAATGTG
                                                                                                                                                                                                                                           ATCCACCGTTCACGTTAAGCGATCTGAAGAAAGCGATTCCTACCCATTGCTTTGAGCGAT
                                                          TTTACTGGTTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG
                                                                                              ATGTAGCCGCCACTTACTTCCACCATCTGCCAAACCCTTTCTCCTCCCTTGCGTGGCTGG
                                                                                                                                                       CCCTTATCCGTTCCTTCTTATGTCGTTTATGACCTTGCTGTGAGCTTCCTCCTCTACT
                                                                                                                                                                                  CTGTCATCCGGTCATCATACTATGTTCTTCATGATCTCATTGTTGCCTATGTCTTCTACT
                                                                                                                          ACCTTGCAAACACGTATATCCCTCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG
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                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 6.8e-102;
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RESULT 11
AAZ32636
ID AAZ32636
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                                                                                                  Fatty acyl dehydrogenase; FAD2; fatty acyl hydroxylase; LFAH12; homology; evolutionarily conserved; wild-type; mutation; oleic acid; linoleic acid; unsaturated fatty acid; ricinoleic acid; oil; wax;
                                                                                                                                                                                                            19-JAN-2000
                                                                                                                                                                                                                                                                               AAZ32636 standard; cDNA;
                                                  Arabidopsis thaliana.
                                                                                    hydroxylated
                                                                                                                                                                     Arabidopsis thaliana wild-type fatty acyl desaturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACTCCGTTTTACGTAGCAATATGGAGAGAGGCAAAGGAGTGTCTGTTCGTGGATCCAG
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                                                                                    fatty acid;
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Location/Qualifiers
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                                                                                                                                                                                                          entry)
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                                                                                    lubricant; nylon; mutant;
                                                                                                                                                                                                                                                                               ВP
                                                                                    mutation;
                                                                                                                                                                        FAD2 cDNA
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Best Local S
Matches 685
                                                                                                                                                                                                                                                                                                                                                                                                                             including castor (Ricinus communis) and the crucifer Lesquerella fendleri. Ricinoleic acid is synthesised by hydroxylation of oleic acid by fatty acyl hydroxylateses (FAHS) which have similar enzymatic properties and which exhibit a high degree of homology to fatty acyl desaturases (FADS). This indicates that FADs and FAHS are evolutionarily related. Seven mutations (A63V, A104G, T148N, Y217F, A295V, S32A and M324I) in the Arabidopsis thaliana FAD2 protein conferred FAH activity upon the mutant FAD protein (AAY50098). Most plant species that are grown for production of oils do not produce significant amounts of hydroxylated fatty acids. Transgenic plants (particularly temperate oilseed crops) that contain mutant FAD or FAH may be used to produce oils, waxes and other fatty acid-based products with altered fatty acid composition. A particular use is increasing content of ricinoleic acid, used in production of lubricants and some forms of nylon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents Arabidopsis thaliana wild-type fatty acyl desaturase FAD2 cDNA. All plants contain one or more fatty acyl desaturases which catalyses the O2-dependent insertion of a double bond between carbons 12 and 13 of lipid-linked oleic acid (18:1) to produce linoleic acid (18:2). By contrast only 14 species in ten plant families have so far been found to accumulate the structurally related hydroxy fatty acid, ricinoleic acid (D-12-hydroxyoctadec-cis-9-enoic acid),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9953073-A2
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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05-MAR-1999;
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SHANKLIN J.
WHITTLE E J.
SOMERVILLE C.
GTCACCATGCATTTAGCGACTACCAGTTGATTGATGACATTGTTGGATTCGTGCTCCATT
                                                                                                                                                                                           CAATCCCTCGCTCTTTCTCCTACCTTATCAGTGACATCATTATAGCCTCATGCTTCTACT
                                                                                                                                                                                                                                                                                       ATCCACCGTTCACGTTAAGCGATCTGAAGAAAGCGATTCCTACCCATTGCTTTGAGCGAT 168
                                                                                                                                                  ACCTTGCAAACACGTATATCCCTCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG
                                                                                                                                                                                                                                                              AACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATCCCGGCGCATTGTTTCAAACGCT 142
                                                                                                                                                                                                                                                                                                                                                                                               1152 BP;
                                                      TCTATTGGGCCTGTCAAGGCTGTGTCCTAACTGGTATCTGGGTCATAGCCCACGAATGCG
                                                                          TTTACTGGTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG
                                                                                                                        ACGTCGCCACCAATTACTTCTCTCTCCTCCCTCAGCCTCTCTTACTTGGCTTGGCCAC
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99US-0123168P
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/product= "Wild-type Arabidopsis thaliana FAD2"
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Pred. No. 7.9e-102;
0; Mismatches 385;
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AACC	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 8 8 8 8
ULT 12 (39493 AAC39493; 17-OCT-2000 (first entry) Arabidopsis thaliana DNA fragment SEQ ID NO: 24835. Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana. Ep1033405-A2.		323 GTCACCACGCATTCAGCGACTACCAATGGCTGGATGACACAGTTGGTCTTATCTTCCATT 382 409 CGGCTCTCCTCACCCCGTATTTCTCTTGGAAATATAGCCACAGGAATCACCACGCCAACA 468
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Best Local Sim
Matches 688;
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24-SEP 1999

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Similarity 63.8%;
88; Conservative
                                                               TTTACTGGTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG
                                                                                                                                                                             ACCTTGCAAACACGTATATCCCTCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG
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                             CTGGATCCCTCGAAAGAGTATTTTGTCCCAAAGCAGAAATCAGCAATCAAGTGGT
                                        CARATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTCAAGATTT
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Pred. No. 8.5e-102;
0; Mismatches 390;
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RESULT 13
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Query Match Best Local

Match 35.3%; Local Similarity 63.8%;

Score 454; DB 2; Pred. No. 1e-101;

Length 2973;

Sequence 2973

BP; 762 A; 637 C; 569

G; 1005 T; 0 U; 0 Other;

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The gene corresp. to AAQ66068 was isolated by screening Arabidopsis genomic DNA library using radiolabeled pSF2b cDNA insert, purifying positively-hybridising plaque, and subcloning a 6kb Hind III insert fragment from the phage DNA in pBluescript vector. Comparison of the sequences of the gene (AAQ66074) and the cDNA (AAQ66068) revealed the presence of a single intron of 1134 bp at a posn. between nucleotides 88 and 89 or the cDNA, which is 4 nucleotides 5' to the initiation codon. The cDNA is contained in clone AAP92103. Plasmid AAP92103 was deposited on October 16, 1992 with the ATCC and bears accession number ATCC 69095. An isolated nucleic acid fragment where in the nucleic acid identity is 90% or greater to AAQ66068 or AAQ66074 is claimed. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                 Claim 3; Page 136-138; 147pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lightner JE,
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S 뭥 Ś В S В S 밁 δ 문 δ 밁 Ş 밁 Ş B S 밁 S 밁 S Matches 2221 2161 2101 2041 1981 1921 1861 1801 469 409 349 289 169 688; ATCCACCGTTCACGTTAAGCGATCTGAAGAAAGCGATTCCTACCCATTGCTTTGAGCGAT 168 CCGATTTCGGTCTTCTCGCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAAAGGGG ACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTGCTAT 708 TCGGGTGGCCCTTGTACTTAGCCTTTAACGTCTCTGGCAGACCGTATGACGGGTTCGCTT TAGGATTTCCGTTATACCTCTTAACTAATATCTCGGGCAAGAAATACGGGAGGTTTGCCA 648 ACGGGAAATACCTCAACAACCCTCTTGGACGCATCATGATGTTAACCGTCCAGTTTGTCC ATTCCAAACTTCTTAACAATCCACCCGGGCGAGTGTTCACTTTGGTGTTTCGGTTGACTT 588 CTGGATCCCTCGAAAGAGATGAAGTATTTGTCCCAAAGCAGAAATCAGCAATCAAGTGGT CAPATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTCAAGATTT CCTTCCTCCTCGTCCCTTACTTCTCCTGGAAGTATAGTCATCGCCGTCACCATTCCAACA CGGCTCTCCTCACCCCGTATTTCTCTTGGAAATATATAGCCACAGGAATCACCACGCCAACA GTCACCACGCATTCAGCGACTACCAATGGCTGGATGACACAGTTGGTCTTATCTTCCATT GTCACCATGCATTTAGCGACTACCAGTTGATTGATGACATTGTTGGATTCGTGCTCCATT TCTATTGGGCCTGTCAAGGCTGTGTCCTAACTGGTATCTGGGTCATAGCCCACGAATGCG TTTACTGGTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG ACCTTGCAAACACGTATATCCCTTTATTCCTACACCTTCTGGCTTACCTTAGCATGGCCCG 288 CAATCCCTCGCTCTTTCTCCTACCTTATCAGTGACATCATTATAGCCTCATGCTTCTACT CTGTCATCCGGTCATCATACTATGTTGTTCATGATCTCATTGTTGCCTATGTCTTCTACT AACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATCCCGCCGCATTGTTTCAAACGCT Conservative 0; Mismatches 390; Indels 0; Gaps 2280 528 468 228 1800 2340 2100 2040 408 1980 1860

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CTGATGCGGGTATTCTAGCCGTCTGTTTTGGTCTTTACCGTTACGCTGCTGCACAAGGGA

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RESULT 14
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15-OCT-1993;
20-JUN-1994;
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                                                                                     Lightner JE,
Yadav NS;
     WPI; 2002-392229/42.
P-PSDB; ABB80027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACTCCAATTTTCAAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCCG 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAGGTG 1186
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                                                                                                                     Okuley
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93WO-US009987.
94US-00262401.
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1659. .1661
/*tag= c
/note= "this represents the ATG start codon for the delta
-12 desaturase gen, the cDNA for which is given in record
ABL58599"
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New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase for creating transgenic plants and producing seed oil with altered levels of unsaturated fatty acids.

Claim 1; Col 99-102; 54pp; English.

CC comprising a sequence encoding a plant enzyme that is a delita-12 cc comprising a sequence encoding a plant enzyme that is a delita-12 cc comprising nucleic acids of the invention are used to cc chimeric genes comprising nucleic acids of the invention are used to cc reate transgenic plants with altered levels of unsaturated fatty acids, and can modify plant lipid composition. Nucleic acids of the invention cc can be used as hybridisation probes to isolate or amplify nucleotide sequences encoding other fatty acid desaturases or fatty acid desaturase. They can also be used in restriction fragment length collymorphism (RFLP) breeding to obtain altered levels of oleic acids in collymorphism (RFLP) breeding to obtain altered levels of oleic acids in collidate oil of oil producing plant species. They can also be used to produce seed oil containing altered levels of unsaturated fatty acids. Nucleic caids of the invention can combine the high oleate trait of transformed cc seeds with mutations for altered fatty acid compositions to obtain new fatty acid compositions and/or improved agronomy. A vegetable oil low in contain sequence in the benefits to consumers (reduced risk of coronary heart disease) as creptesents a cress genomic fragment containing microsomal delta-12 cheafthy acid containing microsomal delta-12 represents a cress genomic desaturase gene to an isolated nucleic acid fragment encoding õ

Sequence 2973 BP; 762 A; 637 C; 569 G; 1005 T; O U; O Other;

Matches Query Match Local 109 688; h 35.3%; Similarity 63.8%; 88; Conservative 0 Score 454; DB 6; Pred. No. 1e-101; 0; Mismatches 390 390; Length 2973; Indels 0 Gaps 168

밁 S 밁 Ş 밁 Ś 밁 5 밁 S 밁 Ś 밁 Ś 문 S 밁 Ś 밁 Ś 2221 2101 2041 1981 1921 1861 1801 469 589 409 349 169 649 289 229 GTCACCACGCATTCAGCGACTACCAATGGCTGGATGACACAGTTGGTCTTATCTTCCATT GTCACCATGCATTTAGCGACTACCAGTTGATTGATGACATTGTTGGATTCGTGCTCCATT ACCTIGCAAACACGTATATCCCTCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG 288 CAATCCCTCGCTCTTTCTCCTACCTTATCAGTGACATCATTATAGCCTCATGCTTCTACT GCCATTTCTTCCCCAACGCTCCCATCTACAATGACCGAGAACGCCTCCAGATATACCTCT TCTATTGGGCCTGTCAAGGCTGTGTCCTAACTGGTATCTGGGTCATAGCCCACGAATGCG TTTACTGGTTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG ACGTCGCCACCAATTACTTCTCTCTCCTCCCTCAGCCTCTCTTACTTGGCTTGGCCAC CTGTCATCCGGTCATCATACTATGTTGTTCATGATCTCATTGTTGCCTATGTCTTCTACT ACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTGCTAT TCGGGTGGCCCTTGTACTTAGCCTTTAACGTCTCTGGCAGACCGTATGACGGGTTCGCTT TAGGATTTCCGTTATACCTCTTAACTAATATCTCGGGCAAGAAATACGGGAGGTTTGCCA ACGGGAAATACCTCAACAACCCTCTTGGACGCATCATGATGTTAACCGTCCAGTTTGTCC ATTCCAAACTTCTTAACAATCCACCCGGGCGAGTGTTCACTTTGGTGTTTCGGTTGACTT CTGGATCCCTCGAAAGAGATGAAGTATTTGTCCCAAAGCAGAAATCAGCAATCAAGTGGT CAAATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTCAAGATTT CCTTCCTCCTCGTCCCTTACTTCTCCTGGAAGTATAGTCATCGCCGTCACCATTCCAACA CGGCTCTCCTCACCCCGTATTTCTCTTGGAAATATAGCCACAGGAATCACCACGCCAACA 468 528 2100 348 228 1800 2340 708 2280 2220 2040 408 1980 1920 1860

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Best Local Similarity 63.7%;
Matches 687; Conservative
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Ş	949	TCCACGACGTTACACACACTCACGTCTTGCATCATTTGATCTCATACATTCCACATTATC 1008
뭉	1075	1075 TCCACAACATTACAGACACACACGTGGCTCATCACCTGTTCTCGACAATGCCGCATTATA 1134
Ş	1009	ATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTTGGGCGAGTACTATAAAATCGACA 1068
용	1135	1135 ACGCAATGGAAGCTACAAAGGCGATAAAGCCAATTCTGGGAGACTATTACCAGTTCGATG 1194
8	1069	1069 GGACTCCAATTTTCAAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCCG 1128
뮍	1195	GAACACCGTGGTATGTGGCGATGTATAGGGAGGCAAAGGAGTGTATCTATGTAGAACCGG 1254
ठ	1129	ATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAAGGTG 1186
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Search completed: June 23, 2004, 13:00:22 Job time: 430 secs

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33.0	33.1	33.1	33.1	33.1	33.1	33.1	33.2	33.2	33.2	33.2	33.2	33.2	33.3	33.3	33.3	33.4	33.4
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US-08-907-608-5	US-09-995-297-1	US-09-966-888-1	US-09-482-287-1	US-09-128-602B-1	US-09-354-231B-1	US-08-907-608-1	US-09-995-297-17	US-09-995-297-15	US-09-128-602B-17	US-09-128-602B-15	US-09-354-231B-17	US-09-354-231B-15	US-09-995-297-13	US-09-128-602B-13	US-09-354-231B-13	US-09-995-297-11	US-09-128-602B-11
Sequence 5, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 15, Appl	Sequence 17, Appl	Sequence 15, Appl	Sequence 17, Appl	-	•	•	•	Sequence 11, Appl	•					

ALIGNMENTS

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; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Crepis alpina
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1125)
US-09-161-994A-1
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US-09-161-994A-1
; Sequence 1, Application US/09161994A
; Patent No. 6333448
; GENERAL INFORMATION:
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APPLICANT: STYMME, Sten
APPLICANT: LENMAN, MARIE
TITLE OF INVENTION: NOVEL PLANT ENZYME AND US)
FILE REFERENCE: BAFOR-1
CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.0
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SEQ ID NO 1
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APPLICANT:
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184
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BANAS, Antoni
DAHLQVIST, Anders
GUMMESON, Per-Olov
                                                                                      GTCATCCGGTCATCATACTATGTTGTTGATGATCTCATTGTTGCCTATGTCTTCTACTAC 230
                                                                                                                              GTAATCCGTTCCTACTACATAGTCCACGATGCTATATCGCCTACATCTTCTACTTC
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RESULT 2
US-09-059-769-1
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Green, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 20
                                                                                                                                                                     Sequence 1, Application US/09059769
Patent No. 6329518
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Best Local Similarity
Matches 903; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (303) 499-8089
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                               CCTTGAACGTGTGCCAGTCGATCC---ACCGTTCACGTTAAGCGATCTGAAGAAAGCGAT 145
                                          TCTGGCTTACCTAGCATGGCCCGTTTACTGGTTTTGTCAAGCTAGCATCCTCACCGGCCT
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78.2%;
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Pred. No. 2.7e-197;
0; Mismatches 237;
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RESULT 3
US-09-059-769-3
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                                                              GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Plant Fatty Ac
TITLE OF INVENTION: Therefor
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                                                                                                                                                                                       Sequence 3, Application US/09059769 Patent No. 6329518
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Circle, Suite 201
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                                                                                                                                                                                                                                                                                                                                                                              GGAATGCATCTACATCGAGCCCGATGAGGATAGCGAGCACAAAGGTGTGTTTCTGGTACCA 1165
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NAME/KEY:
LOCATION:
US-09-059-769-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1312 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 870; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
APPLICATION NUMBER: US 60/050403
APPLICATION TUPENATION:
APPLICATION TUPENATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Crepis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
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Colorado
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                    GITGATTGATGACATTGTTGGATTCGTGCTCCATTCGGCTCTCCTCACCCCGTATTTCTC 433
                                                                                                                                                                                     TATTCCTACACCTCTGGCTTACCTAGCATGGCCCGTTTACTGGTTTTGTCAAGCTAGCAT
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                                                                                                                                                       TCTCCCTCATCCTCTAGCCTAGCTTAGCTTGGCCGCTTTACTGGTTCTGTCAAGCTAGCGT
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78.6%;
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Pred. No. 2.7e-194;
0; Mismatches 228;
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414

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174 193

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RESULT 4
US-08-872-302-3
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Patent No. 5846784
GENERAL INFORMATION:
APPLICANT: Hitz, William D
                                                                                                                                                                                                   TITLE OF INVENTION: Fatty Acid Modifying Enzymes From TITLE OF INVENTION: Developing Seeds of Vernonia galamenensis NUMBER OF SEQUENCES: 10
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                         ZIP: 19898
                                                                                      COUNTRY:
                                                                                                           STATE: Delaware
                                                                                                                          STREET: 1007 Marl
                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                             E: E.I. duPont de Nemours
1007 Market Street
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; LOCATION:
US-08-872-302-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1i MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/872,302 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Majarian, William REGISTRATION NUMBER: P-4 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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     GGGCAGCTTGGGTAATCAACATGTACGCAATTCCAGTACTAGGTGTAAGCGTGTTCTTCG
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                                                            TATCCGATTTCGGTCTTCTCGCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAAAG
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                                       TATCGGATGTGGGTCTCATTGCTGTGTTTTACGGGCTTAAGTTTCTTGTAGCGAAAAAAG
                                                                                                           CCAACCACTTTGATCCGTTGAGCCCCATCTTCAGTGAGCGTGAACGAATCCAGGTCGTGC
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Pred. No. 1.1e-192;
0; Mismatches 277;
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APPLICANT: SOMENUILLE, CHRIS
APPLICANT: SOMENUILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES 7
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND INVENTE OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,596
FILING DATE: 26-SEP-194
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOYULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206905/122/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
             TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1231 base pairs
                                                                                                                                                                                                                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
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                                           ATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTGGGCGAGTACTATAAAATCGACA 1068
                                                                                  TCCACGACGITACACACACTCACGTCTTGCATCATTTGATCTCATACATTCCACATTATC 1008
                                                                                                                                                                                            ACTGGATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTCCTGAATCGGGTTT
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                ACGCAATGGAAGCTACAAAGGCGATAAAGCCAATTCTGGGAGACTATTACCAGTTCGATG 1014
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Pred. No. 5.4e-122;
0; Mismatches 389;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,982
FILING DATE: 11-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/314,596
FILING DATE: 26-SEP-1994
ATTORNEY/ACENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206905/122
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1231 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF FLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                           ATCCACCGTTCACGTTAAGCGATCTGAAGAAAGCGATTCCTACCCATTGCTTTGAGCGAT 168
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     TCTATTGGGCCTGTCAAGGCTGTGTCCTAACTGGTATCTGGGTCATAGCCCACGAATGCG
                              TTTACTGGTTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG
                                                                                                                                                CAATCCCTCGCTCTTCTCCTACCTTATCAGTGACATCATTATAGCCTCATGCTTCTACT
                                                                                                                                                                                  CTGTCATCCGGTCATCATACTATGTTGTTCATGATCTCATTGTTGTCTATGTCTACT
                                                                          ACGTCGCCACCAATTACTTCTCTCTCTCCCTCAGCCTCTCTTACTTGGCTTGGCCAC
                                                                                                            ACCTTGCAAACACGTATATCCCTCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG
                                                                                                                                                                                                                      AACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATCCCGCCGCATTGTTTCAAACGCT
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1100 NEW YORK AVENUE, N.W.
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Pred. No. 5.4e-122;
0; Mismatches 389;
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                                                                                                                                                                                                     Sequence 44, Application Patent No. 6028248
                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OP INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES
TITLE OP INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND
NUMBER OF SEQUENCES: 48
CORRESPONDERGE ADDRESS:
ADDRESSE: PILLSBURY MADISON & SUTRO L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
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COMPUTER READABLE FORM:

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US-08-819-037-44
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CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICTOSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,037
FILING DATE: 11-MRR-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR PRIOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
PRIOR PRIOR DATA:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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TYPE: nucleic acid
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                                                                       GÉCATTTCTTCCCCAACGCTCCCATCTACAATGACCGAGAACGCCTCCAGATATACCTCT
                                                                                                           ACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTGCTAT
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Pred. No. 5.4e-122;
0; Mismatches 389;
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                                                               US-09-045-940-44
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
                                                                                                                                                                           FILING DATE: 26-SEP-1994
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION UNMBER: 08/320,982
PILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23-MAR-19
                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Microsoft Word
                                                                                                 TOPOLOGY:
                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 11
                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44, Application US/09045940
o. 6433250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAGGATAGCGAGCACAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAGGTG 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCACGACGTTACACACACTCACGTCTTGCATCATTTGATCTCATACATTCCACACTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGGGAAGGTGACAAGAAAGGTGTGTACTGGTACAACAATAAGTTATGAGCATGATG 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACACCGTGGTATGTAGCGATGTATAGGGAGGCAAAGGAGTGTATCTATGTAGAACCGG
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                                                                                                                                                           1231 base pairs
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1100 NEW YORK AVENUE, N.W.
                                                                                                      linear
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35.5%;

Score 455.6; DB 4; Pred. No. 5.4e-122;

Length 1231;

Matches

689;

Conservative

0;

Mismatches 389; Indels

0

Gaps

175

229 115

355 409 295 349 235 289

469

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55 AACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATCCCGCCGCATTGTTTCAAACGCT 114
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                                  ATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAAGGTG 1186
                                                                                                                                       GGACTCCAATTTCAAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCCG 1128
                                                                                                                                                                                                                                           ATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTGGGCGAGTACTATAAAATCGACA 1068
                                                                                                                                                                                                                                                                                                                                                TCCACGACGTTACACACACACTCACGTCTTGCATCATTTGATCTCATACATTACCACACATTATC 1008
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          ACAGGGAAGGTGACAAGAAAGGTGTGTACTGGTACAACAATAAGTTATGAGCATGATG
                                                                                                            GAACACCGTGGTATGTAGCGATGTATAGGGAGGCAAAGGAGTGTATCTATGTAGAACCGG
                                                                                                                                                                                                              ACGCAATGGAAGCTACAAAGGCGATAAAGCCAATTCTGGGAGACTATTACCAGTTCGATG 1014
                                                                                                                                                                                                                                                                                                                   TCCACAACATTACAGACACACACGTGGCTCATCACCTGTTCTCGACAATGCCGCATTATA
                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGGCTCAGGGGAGCTTTGGCTACCGTAGACAGAGACTACGGAATCTTGAACAAGGTGT
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US-09-133-962A-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        Matches 689;
                                                                                                                                                                                                                                                                                                                Query Match 35.5%;
Best Local Similarity 63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WIN
SOFTWARE, MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/133,962A
FILLING DATE: 14-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/977,339
FILLING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION
INFORMATION TOWNS
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 93..1244
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1043-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)992-5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENZYMES FROM PLANTS NUMBER OF SEQUENCES: 17
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JOHN JOSEPH OKULEY
TITLE OF INVENTION: GENES FOR MICROSOMAL
DELTA-12 DESATURASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                               229
ACCTTGCAAACACGTATATCCCTCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG
                                                                                                                                                                                      AACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATCCCGCCGCCATTGTTTCAAACGCT
                                                                                                                                                                                                                                      ATCCACCGTTCACGTTAAGCGATCTGAAGAAAGCGATTCCTACCCATTGCTTTGAGCGAT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WILMINGTON STATE: DELAWARE
                                                                                    CAATCCCTCGCTCTTTCTCCTACCTTATCAGTGACATCATTATAGCCTCATGCTTCTACT
                                                                                                                                    CTGTCATCCGGTCATCATACTATGTTGTTCATGATCTCATTGTTGCCTATGTCTTACT
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TELEFAX: (302)773-0164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                   Score 455.6; DB 4;
Pred. No. 5.7e-122;
0; Mismatches 389;
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Sequence 1, Application US/08872302
Patent No. 5846784
GENERAL INFORMATION:
APPLICANT: Hitz, William D
TITLE OF INVENTION: Fatty Acid Mo-
TITLE OF INVENTION: Developing Se
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                             RESULT 10
US-08-872-302-1
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                                                                                                                                                                                                                                           ACAGGGAAGGTGACAAGAAAGGTGTGTACTGGTACAACAATAAGTTATGAGCATGATG
                                                                                                                                                                                                                                                                                ATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAAGGTG
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                                          Seeds
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; LOCATION:
US-08-872-302-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRIGTH: 1476 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-4926
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NAME: Majarian, William R
REGISTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: B.I. duPont de Nemours
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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    TAGGCTGGCCCTTGTACTTGGTTTTCAATGTATCAGGGAGACCCTATGACCGTTTTGCCT
                                      TAGGATTTCCGTTATACCTCTTAACTAATATCTCGGGCAAGAAATACGGGAGGTTTGCCA
                                                                               ACTCAAAATACTTTAACAACGCACCTGGCCGCATGATGAGTGTGTTCACCACCCTAACTC
                                                                                                                                                                                                  CAAATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTCAAGATTT
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nilarity 64.2%;
Conservative
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Pred. No. 1.3e-121;
0; Mismatches 381;
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RESULT 11
US-09-133-962A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JONATHAN EDWARD LIGHTNER
JOHN JOSEPH OKULEY
TITLE OF INVENTION: GENES FOR MICROSOMAL
DELTA-12 DESATURASES
ENZYMES FROM PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1129
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NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-
TELECOMMUNICATION INFORMATION:
                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/133,962A
FILING DATE: 14-AUg-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE E. I. DU PONT DE NEMOURS
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                        MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR 1
SOFTWARE: MICROSOFT WORD VERSION 7.0A
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JOCATION: 521..1654

SEQUENCE DESCRIPTION: SEQ ID
US-09-133-962A-15
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2973 base pairs
TYPE: nucleic acid
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ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: pAGF2-6
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                                                                                              GCCATTTCTTCCCCAACGCTCCCATCTACAATGACCGAGAACGCCTCCAGATATACCTCT
                                                                                                                    ACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTTGCTAT
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                     CTGATGCGGGTATTCTAGCCGTCTGTTTTGGTCTTTACCGTTACGCTGCACAAGGGA
                                                          CCGATTTCGGTCTTCTCGCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAAAGGGG 768
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TELEFAX: (302)773-0164
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Pred. No. 2.5e-121;
); Mismatches 390;
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RESULT 12
US-08-314-596-43
                                                           ; MOLECULE TYPE: US-08-314-596-43
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND
NUMBER OF SEQUENCES: 48
                                                                                                                                                                     TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: KOKILIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 2069
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/314,59)
FILING DATE: 26-SEP-1994
CLASSIFICATION: 435
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CUSHMAN DARBY & CUSHMAN L.L.P.
ADDRESSEB: CUSHMAN DARBY & CUSHMAN L.L.P.
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COUNTRY: U.S.A.
ZIP: 20005
                                                                                             LENGTH: 1222 base p
TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
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33.6%;
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Score 432.4; DB 1;
Pred. No. 2.8e-115;
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               Length 1222;
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                     ATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAGGTGTA 1188
                                                                         GTACCCCATTTTACAAGGCATTGTGGAGGGAGGCAAAGGAGTGCTTGTTCGTCGAGCCAG 1074
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US-08-320-982-43
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Patent No. 58
                                                                                                                                                                                                                                                            Query Match 33.6
Best Local Similarity 61.3
Matches 716; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/314
APPLICATION NUMBER: US 08/314
APPLICATION NUMBER: US 08/314
AFTORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
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SEQUENCE CHARACTERISTICS:
LENGTH: 1222 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
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                                                                                  ACCTTGCAAACACGTATATCCCTCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG
                                                                                                                         CTTTTGTGCGCTCATTCTCCTATGTTGCCTATGATGTCTGCTTAAGTTTTCTTTTCTACT
                                                                                                                                                   CTGTCATCCGGTCATCATACTATGTTGTTCATGATCTCATTGTTGCCTATGTCTTCTACT
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                                                       CGATCGCCACCAACTTCTTCCCTTACATCTCTTCTCCGCTCTCGTATGTCGCTTGGCTGG
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                                                                                                                                                                                                                                                            Score 432.4; DB 1;
Pred. No. 2.8e-115;
0; Mismatches 446;
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                                                                     RESULT 14
US-08-819-037-43
   Sequence 43, Application Patent No. 6028248 GENERAL INFORMATION: APPLICANT: SOMERVILLE
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                                                                                                                                           GTGTTCTAATAAAAAAGGCAAAAAAAAA
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Best Local Similarity Matches 716; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1222 base pair:
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APPLICATION NUMBER: US/CENTRO DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VAN DE LO.
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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1100 NEW YORK AVENUE, N.W.
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BE OF PLANT FATTY ACYL HYDROXYLASES

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Pred. No. 2.8e-115;
0; Mismatches 446;
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Patent No. 6433250
                                                         ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: MICCOSOft WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND
    CLASSIFICATION:
                     APPLICATION NUMBER: US/09/045,940 FILING DATE: 23-MAR-1998
                                                                                                                                                                                                                     STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                 ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P. STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                      COUNTRY: U.S.A.
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APPLICATION NUMBER: 08/320,982
FILING DATE: 11-OCT-194
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/314,596
FILING DATE: 26-SEP-1994
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1222 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TODOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.6%;
Best Local Similarity 61.3%;
Matches 716; Conservative
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ACTGGATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCCGGGTTCCTGAATCGGGTTT
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Sequence 14778, A
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Sequence 3, Appli
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US-09-981-124-1

GENERAL INFORMATION:

Sequence 1, Application US/09981124 Patent No. US20020166144A1

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ALIGNMENTS

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APPLICANT: Green, Allan
APPLICANT: Lenman, Marit
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APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
TITLE OF INVENTION: FATTY ACID METABOLISM
FILE REFERENCE: 26-98A
CURRENT APPLICATION UNMER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1998-04-14
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PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1358
TYPE: DNA
ORGANISM: Crepis palaestina
FEATURE:
NAME/KEY: CDS
LOCATION: (30)..(1151)
COTHER INFORMATION:
US-09-981-124-1
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Query Match

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NAME/KEY: misc feature

( NAME/KEY: misc feature

( COATION: (937)...(937)

( OTHER INFORMATION: N is any nucleotide residue

( NAME/KEY: CDS

( NAME/KEY: misc feature

( CCATION: (901)...(901)

( OTHER INFORMATION: N is any nucleotide residue

US-09-981-124-3
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TITLE OF INVENTION: FATTY ACID METABOLISM
FILE REFERENCE: 26-98A
CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR APPLICATION NUMBER: AU P06223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU P06226
PRIOR APPLICATION NUMBER: AU P06236
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
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US-09-981-124-3
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09981124
Patent No. US20020166144A1
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.9
Best Local Similarity 78.6
Matches 870; Conservative
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ORGANISM: Crepis
FEATURE:
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                        TATTCCTACACCTCTGGCTTACCTAGCATGGCCCGTTTACTGGTTTTTGTCAAGCTAGCAT 313
                                                                                                                                                                                         GAAGCAAGCAATCCCTCCACATTGCTTCCAGCGATCTGTCATCCGTTCATCTTATTACGT
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TCTCCCTCATCCTCTAGCCTACTTAGCTTGGCCGCTTTACTGGTTCTGTCAAGCTAGCGT
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78.6%;
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Pred. No. 1.7e-181;
0; Mismatches 228;
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US-09-981-124-19
; Sequence 19, Application US/09981124
; Patent No. US20020166144A1
; GENERAL IMPORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES
TITLE OF INVENTION: FATTY ACID METABOLISM
FILE REFERENCE: 26-98A
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                                        THEREFOR
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; LOCATION: (44)..(1195)
; OTHER INFORMATION:
US-09-981-124-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR PILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 839; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Vernonia
FEATURE:
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    AGGGGCAGCTTGGGTAATCAACATGTACGCAATTCCAGTACTAGGTGTAAGCGTGTTCTT
                                                                                                                                          TGCCAACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTT
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                                                                           GCTATCCGATTTCGGTCTTCTCGCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAA 763
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                                      GCTTTCTGATTTTGGTCTCATAGCAGTTGCTTACGTGGTTCGTCAAGCTGTACTGGCTAA
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Pred. No. 7.2e-175;
0; Mismatches 229; Indels
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US-10-425-114-14778
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 14778
LENGTH: 1586
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Best Local S
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ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3028-001-B9_FLI
-10-425-114-14778
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                        TCTACTGGGCTGTCCAAGGTTGCATCCTTACTGGAGTTTGGGTCATTGCCCATGAGTGTG
                                                     TTTACTGGTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG
                                                                                      CTGTTTTCCGCTCATTCTCCTATGTTGTTTACGACCTCACCATAGCCTTCTGCCTCTATT
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Pred. No. 3.6e-121;
0; Mismatches 366;
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US-10-424-599-123945/c
Sequence 123945, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated V
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 123945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u> АТССАЛАССАЛССАЛССАЛССАСССАСТСТТСССССАСТАСТАТАВАНТССЯСА 1068</u>
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TYPE: DNA
ORGANISM: Glycine max
FEATURE:
FOTHER INFORMATION: Clone I
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ATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTGGGCGAGTACTATAAAATCGACA 1068
                                                   TCCACGACGTTACACACACACTCATCTGCATCATTTGATCTCATACATTCCACACTTATC
                                                                                                  ACTGGATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTCCTGAATCGGGTTT
                                                                                                                                 TGATTACATTCTTGCAGCATACTCACCCTGCATTGCCACATTACACTTCCTCTGAGTGGG
                                                                                                                                                 TGATCACATATTTGCACCACACCCATCTCTCACTCCCTCATTATGATTCAACCGAATGGA
                                                                                                                                                                                 TTGCCTGGGTGTGTGTTTATGGAGTTCCATTGCTAGTGGTCAATGGATTTTTGGTGT
                                                                                                                                                                                                     CAGCTTGGGTAATCAACATGTACGCAATTCCAGTACTAGGTGTAAGCGTGTTCTTCGTTT
                                                                                                                                                                                                                               CAGATGCAGGAGTACTTGCAGTATGCTATGGCCTTTTCCGTCTTGCCATGGCAAAAGGAC
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                                                                                                                                                                                                                                                                                                                           TTGGTTGGCCCTTGTACTTGGCTTTAAATGTTTCTGGAAGGCCTTATGATAGATTTGCTT
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                                                                                                                                                                                                                                                                                                                                                                            ACTCTAAATACCTTAACAATCCTCCAGGCAGAGTCCTCACTCTTGCTGTCACCCTCACAC 115;
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                                    TCCATAATATTACAGACACTCATGTAGCACATCACTTGTTCTCCACAATGCCACATTATC
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RESULT 6
US-10-455-800-3
i Sequence 3, Application US/10465800
i Publication No. US20040029283A1
i GENERAL INFORMATION:
i APPLICANT: Fillatti, JoAnne
i TITLE OF INVENTION: Intron Double Stranded RNI
FILE REFERENCE: 16517.266
CURRENT APPLICATION NUMBER: US/10/465,800
i CURRENT APPLICATION NUMBER: US/0/390,186
pRIOR APPLICATION NUMBER: US 60/390,186
pRIOR FILING DATE: 2003-06-21
i NUMBER OF SEQ ID NOS: 55
i SOFTWARE: Patentin version 3.1
i EQ ID NO 3
i LEGUTUM 6220
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; TYPE: DNA
; ORGANISM: Glycine
US-10-465-800-3
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Best Local Similarity
Matches 704; Conserv
ACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTGCTAT 708
                                                                                                                              TAGGATTTTCCGTTATACCTCTTAACTAATATCTCGGGCAAGAAATACGGGAGGTTTGCCA: 648
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                                                                                 TIGGTIGGCCCTIGTACTIGGCTTTAAAIGTTICTGGAAGGCCTTAIGATAGATTIGCTI 5355
                                                                                                                                                                                                                                                                                                      CTGGTTCTCTTGAGCGGGATGAAGTATTTGTGCCAAAGCAGAAGTCCTGTATCAAGTGGT
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Pred. No. 8.1e-121;
0; Mismatches 366;
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US-10-176-149-3
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FILE REFERENCE: 16518.056
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/10/176,149
CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: US 60/151,224
PRIOR APPLICATION NUMBER: US 60/172,128
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: US 60/172,128
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: US 09/638,508
PRIOR PRIOR DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                LENGTH: 6220
TYPE: DNA
ORGANISM: Glycine m
S-10-176-149-3
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                                                                                                                                                                           Query Match 37.7%; Score 484.4; DB 15; Best Local Similarity 65.8%; Pred. No. 8.1e-121; Matches 704; Conservative 0; Mismatches 366;
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                                       CTGTTTTCCGCTCATTCTCCTATGTTGTTTACGACCTCACCATAGCCTTCTGCCTCTATT
                                                         CTGTCATCCGGTCATCATACTATGTTGTTCATGATCTCATTGTTTGCCTATGTCTTCTACT
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RESULT 8
US-10-425-114-12782
; Sequence 12782, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Chou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
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APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERBUCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 12782

LENGTH: 1457
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Best Local :
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ORGANISM: Glycine max
FEATURE:
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Local Similarity 65.6%;
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ACTGGATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTCCTGAATCGGGTTT 948
                                                                                                                                                             CAGATGCAGGAGTACTTGCAGTATGCTATGGCCTTTTCCGTCTTGCCATGGCAAAAGGAC
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                                                            TGATCACATATTTGCACCACACCCATCTCTCACTCCTCATTATGATTCAACCGAATGGA
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                               TGATTACATTCTTGCAGCATACTCACCCTGCATTGCCACATTACACTTCCTCTGAGTGGG
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Pred. No. 2.6e-120;
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CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,124
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Liu, Qing
TITLE OF INVENTION: Method of Modifying the
FILE REFERENCE: 45-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Gossypium
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LOCATION: (98)
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                  CGGCTCTCCCCCACCCCGTATTTCTCTTGGAAATATAGGCCACAGGAATCACCACGCCAACA 468
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                                                                                                  GTCACCATGCATTTAGCGACTACCAGTTGATTGATGACATTGTTGGATTCGTGCTCCATT
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CTTCTCTTAGTTCCATATTTCTCTTGGAAATATAGCCACCGGCGTCACCATTCTAACA
                                                                                                                                       TTTATTGGGCCATGCAAGGTTGCATTTTGACCGGCGTTTGGGTCATAGCCCCATGAATGTG
                                                                                                                                                                        TTTACTGGTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG
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Pred. No. 1.1e-110;
0; Mismatches 392;
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Sequence 3, Application US/09852399
; Sequence 3, Application US/09852399
; Patent NO. US20020045232A1
; GENERAL INFORMATION:
   APPLICANT: Qiu, Xiao
   TITLE OF INVENTION: PRODUCTION OF CONJUGATED
   TITLE OF INVENTION: LINOLENIC ACIDS IN PLAN
   FILE REFERENCE: BNZ-002
CURRENT APPLICATION NUMBER: US/09/852,399
; CURRENT FILING DATE: 2001-05-09
   PRIOR APPLICATION NUMBER: USSN 60/203,027
; PRIOR TILING DATE: 2000-05-09
   NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-852-399-3
                     US-09-852-399-3
                                  SEQ ID NO 3
LENGTH: 1411
TYPE: DNA
ORGANISM: Calendula o
FEATURE:
FEATURE:
LOCATION: (89)...(123
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                                                             GGACTCCAATTTTCAAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCCG
                                                                                                               ATGCAATGGAAGCCACGAAGGTGATCAAACCGATTTTGGGCGATTATTATCAGTTTGACG
                                                                                                                                      ATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTTGGGCGAGTACTATAAAATCGACA 1068
                                                                                                                                                                                       TCCATAACATAACCGACACTCACGTGGCCCACCATTTGTTCTCTACAATGCCTCATTACC
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Pred. No. 2.1e-110;
0; Mismatches 392;
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LENGTH: 1411
; TYPE: DNA
; ORGANISM: GOSSYPIUM SP.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1233)
US-09-837-751-3
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US-09-837-751-3
US-09-837-751-3
; Sequence 3, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
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Best Local
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APPLICANT: Singh, Surinder
APPLICANT: Liu, Qing
TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
FILE REFERENCE: 45-00
CURRENT APPLICATION NUMBER: US/09/837,751
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,124
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 35
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                                            ACCACTTTGATCCCATGAGTCCAATTTTTCAACGATCGTGAACGCGTTCAAGTTTTTGCTAT
                                                                                                                                                                                                                                      CAAATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTCAAGATTT
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                                                                                                                                                  TIGCGAAATACTTAAACAATCCACCCGGTCGAGTTCTATCTCTTGTAGTCACATTGACTC
                                                                                                                                                                                 ATTCCAAACTTCTTAACAATCCACCCGGGCGAGTGTTCACTTTGGTGTTTCGGTTGACTT 588
                    CCCACTATAACCCTTATGGCCCCATTTACTCCGATCGCGAGAGGCTACAAGTTTACATCT
                                                                                                                 TAGGATTTCCGTTATACCTCTTAACTAATATCTCGGGCAAGAAATACGGGAGGTTTGCCA 648
                                                                                                                                                                                                                   CCGGTTCCATGGAGCGTGACGAAGTATTCGTGCCCAAACCCCAAGTCTAAATTATCATGCT
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0; Mismatches 372;
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Publication No. US20030221217A1
GENERAL INFORMATION:
APPLICANT: Saskatchewan Wheat Pool
TITLE OF INVENTION: PLANT FAD2 CODING SEQUENCE BAL
TITLE OF INVENTION: OILS
FILE REFERENCE: 4810-64280;
CURRENT APPLICATION NUMBER: US/10/330,775;
CURRENT FILING DATE: 2002-12-26;
PRIOR APPLICATION NUMBER: CA 2,382,767;
PRIOR APPLICATION NUMBER: CA 2,382,767;
PRIOR PILING DATE: 2002-05-15;
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
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; TYPE: DNA
; ORGANISM: Brassica
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RESULT 13
US-09-995-297-9
J. Sequence 9, Application US/09995297
Patent No. US20020092038A1
GENERAL INFORMATION:
APPLICANT: Kodali, Dharma

APPLICANT: Fan, Zhegong

APPLICANT: DeBonte, Lorin R.

TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN TITLE OF INVENTION: FATTY ACID CONTENT

FILE REFERENCE: 07148-072002

CURRENT APPLICATION NUMBER: US/09/995,297

CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: US 09/128,602

PRIOR FILING DATE: 1998-08-03
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ORGANISM: Brassica
FEATURE:
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 TTCCACGACGTTACACACTCCACGTCTTGCATCATTTGATCTCCATACATTTCCACATTAT
                                                      GATTGGTTGAGGGGAGCTTTGGCCACCGTTGACAGAGACTACGGAATCTTGAACAAGGTC
                                                                                AACTGGATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTCCTGAATCGGGTT
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Pred. No. 1.1e-106;
0; Mismatches 390;
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Sequence 9, Application US/09771904
Publication No. US20030131379A1
GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Fan, Zhegong
APPLICANT: Fan, Zhegong
APPLICANT: Mino, Guo-Hua
TITLE OF INVENTION: FATTY ACID DESATURASES ANI
TITLE TO INVENTION NUMBER: US/09/771,904
CURRENT APPLICATION NUMBER: US/09/771,904
CURRENT FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR APPLICATION DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
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US-09-771-904-9
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ORGANISM: Brassica
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    TCCAAACTTCTTAACAATCCACCCGGGCGAGTGTTCACTTTGGTGTTTCGGTTGACTTTA 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10715100 Publication No. US20040083503A1 GENERAL INFORMATION:
                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 9
Query Match
                                                                                                                                                                                                                                               APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072002
CURRENT APPLICATION NUMBER: US/10/715,100
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US/09/995,297
PRIOR APPLICATION NUMBER: US/09/128,602
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR APPLICATION NUMBER: US 09/128,602
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 68
                                                                NAME/KEY: CDS
LOCATION: (1)...(1152)
                                                                                                           ORGANISM: Brassica napus FEATURE:
                                                                                                                                                     TYPE: DNA
                                                                                                                                                                          LENGTH: 1155
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SUMMARIES

Result No. a 715.88 71 750.4 738 Score Query Match Length 멂 AX089471 COP245938 AY166773 AY166776 AY166777 CAY166777 CAY16277 CAY16283 AX031160 BD061165 BD061165 BD061165 BAY064128 AY064128 AY064128 AY162108 AY162120108 AY162120108 AY162120108 AY162127 AY162127 AY162127 AY162127 AY162127 AY178445 AR207486 Sequence L26296 Arabidopsis AY039572 Arabidops AP002063 Arabidops AC069473 Arabidops AR064127 Sequence AY142057 Arabidops AR207494 Sequence AY084545 Arabidops BD171810 Gene part AB094415 Spinacia AY178445 Trichosan HBD061164 Plant fat Y16283 Crepis pala AR367418 Sequence AX031162 Sequence BD061165 Plant fat AR064128 Sequence AY166778 Helichrys AY462108 Stokesia AP006377 Lotus cor AF074324 Borago of AF525534 Vernicia AF251844 Helianthu AF188264 Vernonia AF251843 Vernonia AY083163 Olea euro AF188264 Vernonia AY083163 Olea euro AF188264 Vernonia AY083163 Olea euro AF182675 Helianthu AF071892 Prunus ar AF071893 Petroselinu Y16284 Crepis pala X92847 S.commerson AR037150 Sequence 165761 Sequence 44 AY166777 Dimorphot Y16285 Crepis alpi AR367437 Sequence AX031160 Sequence BD061164 Plant fat AX089471 Sequence AJ245938 Calendula AY166773 Helianthu AY166776 Rudbeckia Description

ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX089471	RESULT 1
1 Feussner, I., Hornung, E., Fritsche, K., Peitzsch, N. and Renz, A.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae; Calenduleae;	Calendula officinalis	Calendula officinalis		AX089471.1 GI:13443732	AX089471	Sequence 1 from Patent WO0116362.	AX089471 . 1285 bp DNA linear PAT 21-MAR-2001		

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(8,11)-linoleoyl desaturase; des8.11 gene.
(2alendula officinalis
Calendula officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; ebdicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
calenduleae; Calendula.
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Pflanzenbiochemie, Weinberg 3, D-06120 Halle/Saale, GERWANY
Cocation/Qualifiers
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BS Lett. 462 (3), 249-253
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Query Match 89.6%;
Best Local Similarity 100.0%;
Matches 1152; Conservative
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/tissue_type="developing seed"
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2 (bases 1 to 1419)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Helianthus
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Helianthus
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Direct Submission
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/codon_start=1
/product="delta1-fatty acid acetylenase"
/protein_ide="AAO38032.1"
/protein_ide="AAO38032.1"
/db xref="GI:31322135"
/translation="MGAGGRMSDPSEGKNILERVPIDPPFTLSDLKKAIPAHCFERSV
                                                                                                                                                                   Location/Qualifiers
                                                                                              db_xref="taxon:4232"
                                                                                                                   organism="Helianthus/mol_type="mRNA"
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CCCATCTCACTCCCTCATTATGATTCAACCGAATGGAACTGGATCAAAGGCGCCTTAT
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AVYSKLLNNDPGRVFTLVFLTILGFPLYLLTINISGKKYGRFANHFDPLS9IFTBRBRI
QVVISDIGILAVLYATKLLVBAKGAAWYTCMYLLPULGVHMFFVLITYLHHTHLSLBH
YDSTEWNWIRGALSTIDRDFGFLNRVFHDVTHTHVLHHLISYIPHYAKEARDAIKFV
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Pred. No. 4.3e-218;
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AAAGCGATTCCTACCCATTGCTTTGAGCGATCTGTCATCCGGTCATCATACTATGTTT

AAGGCCATCCCGCCCATTGCTTCGAACGATCCGTCATTCGTTCATCGTACTATGTTGTT

60

Query Match Best Local S Matches 835

Similarity

58.4 ilarity 85.3 Conservative

.3%;

Score 750.4; DB 8; Pred. No. 2.3e-186; 0; Mismatches 144;

Length Indels

979;

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Gaps

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835;

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JOURNAL
REFERENCE
AUTHORS
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AY166776
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AUTHORS
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AY166776
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Submitted (19-OCT-2002) Crop Genetics, DuPont, B
Experimental Station, Wilmington, DE 19880-0402,
                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 979)
Cahoon, E.B., Schmurr, J.A., Huffman, E.A. ar Fungal responsive fatty acid acetylenases evolutionarily distant plant families plant J. 34 (5), 671-683 (2003)
2 (bases 1 to 979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rudbeckia hirta
Rudbeckia hirta
Rudbeckia hirta
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Rudbeckia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 979)
            /translation="Kaipphcfersvirssyyvvhdlivayvfyflantyipllptpw

Aylawpvywfcqasiltglwvighecchhafsdyqllddlugfvefhlallftpyfswky

Shruhtjusldnietrfpylltin

Isgkkygrfanhfpdplspiftprekkyvlayldglllaafyaikllvaakgfawvtswy

Lipvmgvhmffvlitylhhthlslphydstemnwikgalstidrdfgflurvfhdvth

Thvlhhlisyiphyhakeardaikpulgefykidrtfifkamwrxakexv"
                                                                                                                    /product="delta12-fatty
/protein_id="AAO38035.1"
/db_xref="GI:31322141"
                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:52299"
                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                            'product="deltal2-fatty acid acetylenase"
                                                                                                                                                                                                                                                                                 organism="Rudbeckia
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                                                                                                                                  GAGGCTAAGGAATGCATCT 1116
                                                                                                                                                                                                                                    CATCATTTGATCTCATACATTCCACATTATCATGCAAAGGAAGCAAGGGATGCAATCAAG
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                                                                                                                  GANGCCAAAGAATGNGTAT
                                                                                                                                                                                 CCAGTGTTGGGCGAGTACTATAAAATCGACAGGACTCCAATTTTCAAAGCAATGTATAGA
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                                                                                                                                                                                                                                                                                                                                                                                            CCAGTACTAGGTGTAAGCGTGTTCTTCGTTTTGATCACATATTTTGCACCCACACCCATCTC
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Best Local Similarity
Matches 825; Conserv
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                                                                             TACATTCCTAAACGTAAGTCGAAGGTCAAGATTTATTCCAAACTTCTTAACAATCCACCC
                                                                                                                                  TGGAAATATAGCCACAGGAATCACCACGCCAACACAAATTCACTCGATAACGATGAAGTT
                                                                                                                                                                                  TTGATTGATGACATTGTTGGATTCGTGCTCCATTCGGCTCTCCTCACCCCCGTATTTCTCT
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              GGTCGAGTCTTTACTTTGGTTTTTAGGTTGACTCTAGGKTTCCCTTTATATCTTTTAACC
                                    GGGCGAGTGTTCACTTTGGTGTTTCGGTTGACTTTAGGATTTCCGTTATACCTCTTAACT
                                                                                                                                                                                                                      CTCACCGGTTTATGGGTGATTGGTCATGAATGTGGTCATCATGCATTTAGTGAACAACAG
                                                                                                                  TGGATTGGTGACACTGTTGGATTCATACTTCATTCTGCTCTCTTTACCCCCTTATTTCTCT
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nilarity 84.4%;
Conservative
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Pred. No. 4.1e-183;
1; Mismatches 149;
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Length 979; Indels

0,

Gaps

314

120

180

254 60

CTTAACAACCCACCC

420

554

494

300 434 240

360

480 614

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KEYWORDS
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Dimorphotheca sinuata
Dimorphotheca sinuata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Calenduleae; Dimorphotheca.
1 (bases 1 to 979)
Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.
Fungal responsive fatty acid acetylenases occur widely in
evolutionarily distant plant families
Plant J. 34 (5), 671-683 (2003)
2 (bases 1 to 979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cahoon, E.B.

Direct Submission

Direct Submission

Submitted (19-0CT-2002) Crop Genetics, DuPont, Bl
Submitted Station, Wilmington, DE 19880-0402,
/product="delta12-fatty acid acetylenase"
/protein_id="AAO38036.1"
/db_xref="G1:31322143"
/ta_halation="KK1PHC/FERSLIRSSYYVVHDLIVAYVFYFLANTYIPLLPAP
/translation="KK1PHC/FERSLIRSSYYVVHDLIVAYVFYFLANTYIPLLPAP
LAYLAMPVYMFCQASILTGLMVIGHECGHHAFSEQQMIGDTVGFILHSALFTPYFSWK
YSHRSHHANTMSLDNDEVYIPKRKSKVRNYSKILNNPFGRVFTLVFRLTLGFPLYLLT
NVSGKYYERFANHFDPMSPIFTERERIQVVLSDLGIIAVCYALKVLVAAKGATWVMCM
YGVPVIGVHAFFVLITYLHHTMLSLPHYDSSEMNWIKGALSTIDRDFGFLNRVFHDVT
HTHVLHHLISYIPHYHAKEARDAIIPVLGEFYKIDRTPIFKAMMREAKEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Dimorphotheca
/mol_type="genomic_DNA"
/db_xref="taxon:112408"
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Direct Submission
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Direct Submission
Submitted (22-DEC-2000) M.A. Lee, Nilsson Ehle Laboratory,
Swebull Ab, S-26881, Svalov, SWEDEN
On Dec 24, 2000 this sequence version replaced gi:3341397.
Con Location/Qualifiers
1. .1435
                                                                                                                                                                                                                                                                            Science : 98239771
                                                                                                                                                     Direct Submission
Submitted (21-JAN-1998) M.A. Lee,
Webull Ab, S-26881, Svalov, SWEDEN
Revised by [4]
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Science 280 (5365), 915-918 (1998)
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Nilsson, R., Liljenberg, C., Dahlqvist, A.,
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DFYKIDRTPILKAMWREAKECIFIEPEKGRGSKGVYWYNKF"
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Green, A., Singh, S., Lenman, M. and Stymne,
Plant fatty acid epoxygenase genes and us
Patent: US 6329518-A 1 11-DEC-2001;
Location/Qualifiers
1. .1358
                                                                                                                                                                                                                                                                                                      Unclassified.
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                                                                                                                                                                  Similarity 78.2
03; Conservative
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                                                                                                                                                                                                                    /organism="unknown"
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                                                                                                                                               GGAATGCATCTACATCGAGCCCGATGAGGATAGCGAGCACAAAGGTGTTGTTCTGGTACCA 1165
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green, A., Singh, S., Stymne, S. and Lenman, M.
Plant fatty acid epoxygenase genes and uses therefor
Patent: WO 9846762-A 1 22-OCT-1998;
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                 CCACAGGAATCACCACGCCAACACAAATTCACTCGATAACGATGAAGTTTACATTCCTAA
                                                                                                              AGCAAGTCCAAACTCGCGCGTATCTATAAACTTCTTAACAACCCACCTGGTCGGCTGTT
                                                                                                                                                             ACGTAAGTCGAAGGTCAAGATTTATTCCAAACTTCTTAACAATCCACCCGGGCGAGTGTT
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/protein_id=CC09644.1"
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/db_xref="GI:10278514"
/db_xref="GI:10278514"
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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N BD061164.1 GI:22606770

PD061164.1 GI:22606770

JP 2001518797-A/1.

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD Spermatophyta; Andropogoneae; Zea.

E 1 (bases 1 to 1358)

S Stymme, S., Green, A., Singh, S. and Lenman, M.

S Stymme, S., Green, A., Singh, S. and Lenman, M.

S Stymme, S., Green, A., Singh, S. and Lenman, M.

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                                                          STYMNE

PN JP 2001518797-A/1

PD 16-OCT-2001

PF 09-APR-1998 JP 1998543302

PF 19-APR-1997 AU

PR 15-APR-1997 US 60/043706,20-JUN-1997 US 60/0:

STYMNE, ALLAN GREEN, SURINDER SINGH, MARIT LENMAN PC

C12N15/53,C12N9/02

CC Strandedness: Single;

CC Topology: Linear;

FH Key

FT CDS

STYMNE, ALLAN GREEN (SURINDER SINGH, MARIT LENMAN PC

C12N15/53,C12N9/02

CC Strandedness: Single;

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Linear;

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/db_xref="taxon:4577"
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78.2%;
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Pred. No. 3e-177;
0; Mismatches 237;
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ATATATCAACAACATGGGTGCTGGTGGTCGGATGTCGGATCCATCTGAGGGAAAAAAACAT

Query Match Best Local S Matches 903

Similarity

55.7%; 78.2%;

Score 715.8; DB 8; Pred. No. 3e-177; 0; Mismatches 237;

Length Indels

15;

Gaps

88

903; 29 AT

Conservative

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Crepis palaestina
Crepis palaestina
Crepis palaestina
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Crepis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-JAN-1998) M.E. I
Research, SLU, Herman Ehles V
Location/Qualifiers
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Science 280 (5365), 915-918 (1)
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/product="delta 12 fatty acid epoxygenase"
/protein_id="CAA76156.1"
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WFLSDLGLLAVFYGIKVAVANKGAAWVACMYGVFULGVFTFFDHTTGLSSPHY
PENENATIOAA GAIDAGGAAWVACMYGVFULGVFTFFDHTTGLSSPHY
                DSTEWNWIRGALSAIDRDFGFLNSVFHDVTHTHVMHHLFSYIPHYHAKEARDAIKPIL
GDFYMIDRTPILKAMWREGRECMYIEPDSKLKGVYWYHKL"
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/clone_lib="lambda ZAP"
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Gummeson,P., Sjoedahl,S.,
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                                  GGAATGCATCTACATCGAGCCCGATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCA
                                                                       GGGCGACTTTTATATGATCGACAGGACTCCAATTTTAAAAGCAATGTGGAGAGAGGGCCAG
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Sequence 3
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Green, A., Singh, S., Lenman, M. and S
Plant fatty acid epoxygenase genes .
Patent: US 6329518-A 3 11-DEC-2001;
Location/Qualifiers
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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enkaryota; Vagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Crepis.
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Sequence 3
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Plant fatty acid epoxygenase genes and uses therefor
Patent: WO 9846762-A 3 22-OCT-1998;
GREEN ALLAN (AU); SINGH SURINDER (AU); COMMW SCIENT
(AU); STYMNE STEN (SE); LENMAN MARIT (SE)
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/db_xref="GI:10278516"
/db_xref="RGI:10278516"
/db_xref="REMTREMBL:CAC09645"
/translation="MGAGGRGRISEKSYMERYSUDPYTFSLSDLKQAIPPHCFQRSVIRSSYYVVQDLIIAYIFYFLANTYIPNLPHPLAYLAWPLYWFCQASVLTGLWILGHECGHAYSSYTWVDDTVGFIIHSFILLTPYFSWKYSHRNHHSNTSSIDDEVYIPKSKSKLKRIYKLLNNPPGRLLVLVIMFTLGPPLYLLTNISGKKYDRFANHFDPMSPIFERFYQVFLSDLGLLAWPYGJKVAVANKGAAWVACMYGVPVLGVFTFPDVITFLHHTHQSSPHYDSTEMNWIRGALSAIDXDFGFLNSVFHDVTHTHVMHHLFSYIPHYHAKEARDAIKPILGDFYMIDRTPILKAMWREGRECMYIEPDSKLKGVYWYHKL"
                                                                                                                                                                                                                                                        /note="unnamed protein product"
/codon_start=1
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   TAGAGAGGCTAAGGAATGCATCTACATCGAGCCCGATGAGGATAGCGAGCACAAAGGTGT 1153
                                                                    CAAGCCAGTGTTGGGCGAGTACTATAAAATCGACAGGACTCCAATTTTCAAAGCAATGTA 1093
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                                     CAAACCGATCTTGGGCGACTTTTATATGATCGATAGGACTCCAATTTTAAAAGCAATGTG
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1 (bases 1 to 1312)

Stymne,S., Green,A., Singh,S. and Lenman,M.

Plant fatty acid epoxygenase genes and uses therefor

Pattern SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN

STYMNE OF AUTOMORPHIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN

OS Crepis sp.

PD 16-OCT-2001

PD 16-OCT-2001

PF 09-APR-1998 JP 1998543302

PF 09-APR-1998 JP 1998543302

PF 09-APR-1997 AU PO 6225 NEW 15-APR-1997 US 60/050403 PI STEN

STYMNE, ALLAN GREEN, SURINDER SINGH, MARRIT LENMAN PC

C12N15/53, C12N9/02

CC TOPOLOGY: Linear;

FH Key Location/Qualifiers

FT CDS

FT CDS

CC TOPOLOGY: Linear;

FT CDS
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                                   GTTGATTGATGACATTGTTGGATTCGTGCTCCATTCGGCTCTCCTCACCCCGTATTTCTC
                                                                  CCTCACTGGGTTATGGATCCTCGGCCATGAATGTGGTCACCATGCCTATAGCAACTACAC
                                                                                                CCTCACCGGCCTCTGGGTCATCGGTCACGAATGTGGTCACCATGCATTTAGCGACTACCA
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/mol_type="genomic DNA"
/db_xref="taxon:137775"
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78.6%;
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Pred. No. 1.6e-174;
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Sequence
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Patent: US 5846784-A 3
                                                                                                Fatty acid modifying enzymes from developing seeds of Vernonia
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                                                                                                                                                                                                                                                                                                                                                                   GTTCTGGTACCACAAGATGTAATCAAA
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                                                                                                                                (bases 1 to 1364)
                       Location/Qualifiers
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/organism="unknown"
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                ACAGGACTCCAATTTTCAAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGC
                                                                           ATCATGCAAAGGAAGCAAGGGATGCAATCAAGCCAGTGTTGGGCGAGTACTATAAAATCG
                                                                                                              TGTTCCATGACGTCACACACACACGTGTTGCATCTTGTTCCCGTACATTCCACATT
                                                                                                                                TTTTCCACGACGTTACACACACACTCACGTCTTGCATCATTTGATCTCATACATTCCACATT
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                                                       ATCATGCAAAGGAGGCGAGCGCAATAAAGCCGGTGTTAGGGGGAGTATCGGATGATCG
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ATAGGACTCCGTTTTACAAAGCAATGTGGAGAGAGGCGAAGGAATGCATCTACATCGAGC
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75.8%;
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Pred. No. 4.8e-173;
D; Mismatches 277;
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JOURNAL REFERENCE
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AUTHORS
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Matches 790
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TITLE
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1 (bases 1 to 979)

1 (bases 1 to 979)

Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E. Fungal responsive fatty acid acetylenases occur widely evolutionarily distant plant families plant J. 34 (5), 671-683 (2003)

2 (bases 1 to 979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-OCT-2002) Crop Gene Experimental Station, Wilmington, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cahoon, E.B.
Direct Submission
Submitted (19-OCT-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helichrysum bracteatum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asteride; campanulide; Asterales; Asteraceae; Asteroideae;
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Helichrysum
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                                                                      STTCAYGATCTTATCRTTACCTTACGTCTTTTACTTACCTCGCRARCACWTACATYCCTMTT
CTCCCRGCTCATCTCGCTTACCTTARCGTGGCCGGTTTATTGGTTTTGTCAAGCTAGTATT
                 ATTCCTACACCTCTGGCTTACCTAGCATGGCCCGTTTACTGGTTTTTGTCAAGCTAGCATC
                                                                                     GTTCATGATCTCATTGTTGCCTATGTCTACTACCTTGCAAACACGTATATCCCTCTT
                                                                                                                                            AAGAAGGCTATMCCTCCTCACTGTTTCGAACGATCTGTTATTCGTTCATCTTACTACGTT
                                                                                                                                                                      AAGAAAGCGATTCCTACCCATTGCTTTGAGCGATCTGTCATCCGGTCATCATACTATGTT
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/product="delta12-fatty acid acetylenase"
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/mol_type="genomic DNA"
/db_xref="taxon:220345"
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ALIGNMENTS

COMMENT	JOURNAL		REFERENCE AUTHORS		ORGANISM	KEYWORDS SOURCE	ACCESSION VERSION	RESULT 1 BQ994479 LOCUS DEFINITION
Contact: Alexander KOZIK [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742	Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/ Unpublished (2002)	Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.	1 (bases 1 to 691) 1 (bases 1 to 691) Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichoriese : Lactica.	Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	EST. Lactuca sativa	GEFFF12, mkNA sequence. BQ994479 BQ99449.1 GI:22414014	BQ994479 691 bp mRNA linear EST 21-AUG-2002 QGF7F12.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone

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Email: akozik@atgc.org [michelmore@vbelongs to contig QG_CA_Contig2502, for details.

Plate: QGF7 row: F column: 12.
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TAG_LIB-QG_ERGHJ lettuce serriola
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/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
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1 (kzik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
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EST.
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GGC7H15.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
QGC7H15, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig2502, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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:e: QGC7 row: H column: 15.
                                                                                                                                                             Conservative
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/clone lib="QG ABCDI lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library the control of RNA and library size bias.
                                                                                                                                                                                                                                                                     construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TISSUB=chemical induction
TAG_LIB=QG_ABCDI lettuce salinas
TAG_SEQ=TGTAGCCGGG"
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'clone="QGC7H15"
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'cultivar="Salinas"
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http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Tel: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig6400, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                         Heliantheae; Helianthus.

1 (bases 1 to 613)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rie Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Ziegle Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Asteroideae;
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Ziegle,J.,
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Matches 485;
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Plate: QHN8
                       TTCGGTTGACTTTAGGATTTCCGTT
                                                                                               AGGTCAAGATTTATTCCAAACTTCTTAACAATCCACCCGGGCGAGTGTTCACTTTGGTGT
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TTAGGTTAACTCTAGGGTTTCCCTT
                                                                           AAGTTGCAGTTTACTCAAAGCTTCTTAACAATCCCCCTGGTCGAGTGTTCACTTTGGTTT
                                                                                                                                                     ACCACGCCAACACGAATTCGCTTGATAACGATGAAGTTTACATTCCTAAACGCAAGGCCA
                                                                                                                                                                         ACCACGCCAACACAAATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGA
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/note="Vector: pGEM-T; The library was constructed from
three different sources (seedling, root and leaf) of NA
from a single genotype. CDMAs were pooled and cloned into
a high-copy vector pGEM-T. Details of library construction
can be obtained at http://cgpdb.ucdavis.edu/"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:73275"
/clone="QHN8F08"
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GI:33135638

EST 22-JUL-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 624)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig3889, see http://cgpdb.ucdavis.edu/
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                                                          GATGCAATCAAGCCAGTGTTGGGCGAGTACTATAAAATCGACAGGACTCCAATTTTCAAA 1089
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                                                                                                                                                                                                          TTATCAACAATCGATAGGGATTTCGGGTTCCTGAATCGGGTTTTTCCACGACGTTACACAC
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     GCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCCGATGAGGATAGCGAGCAC
                                                                                                        ACTCACGTCTTGCATCATTTGATCTCGTACATTCCACATTATCATGCAAAGGAGGCAAGG
                                                                                                                                 ACTCACGTCTTGCATCTTGATCTCATACATTCCACATTATCATGCAAAGGAAGCAAGG
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1-(530)-752-9659
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/note="Vector: pGEM-T; The library was constructed from
three different sources (seedling, road leaf) of RNA
from a single genotype. CDNAs were pooled and cloned into
a high-copy vector pGEM-T. Details of library construction
can be obtained at http://cgpdb.ucdavis.edu/"
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Location/Qualifiers
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/mol_type="mRNA"
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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Flate: QHM8 row: J column: 13.

Plate: Location/Qualifiers
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Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 530)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
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530 bp mRNA linear EST 22-JUL-2003 QHM8J13.yg.abl QH_M sunflower H.argophyllus Helianthus argophyllus CDNA clone QHM8J13, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QH_CA_Contig6400, see http://cgpdb.uc
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EST.
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                                                                                                                                                               CATCTGAGGGCAAAAACATCCTCGAACGTGTCCCCCATTGATCCACCATTCACTCTAAGTG
                                                                                                                                                                                               CATCTGAGGGAAAAAACATCCTTGAACGTGTGCCAGTCGATCCACCGTTCACGTTAAGCG
                                                                                                                                                                                                                                                                      CTCATCTCTGAGGTTATCAAACATCCACCAACATGGGTGCAGGTGGCCGGATGTCAGACC
                                                                                                                                                                                                                                                                                                           CTTCTCTGTGAGGGTAATTATATATATAACAACATGGGTGCTGGTGGTGGTCGGATGTCGGATC
ATGTTGTTCATGATCTCATTGTTGCCTATGTCTTCTACTACCTTGCAAACACGTATATCC
                                                   ATCTAAAGAAAGCAATCCCTGCTCACTGCTTCGAACGATCTGTCATCCGTTCATCTTACT
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/clone_lib="QH_M sunflower H.argophyllus"
/clone_lib="QH_M sunflower H.argophyllus"
/note="Vector: pBRcDNASfiAB; The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. CDNAs were pooled and directionally cloned into a custom medium-copy vector.
Details of library construction can be obtained at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://cgpdb.ucdavis.edu/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:73275"
/clone="QHM8J13"
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84.7%;
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Pred. No. 1.7e-42;
D; Mismatches 74
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//uparishin-boundary /mol type="makNa" /culTivar="Kennebec" /db_xref="taxon:4113" /clone="pOACP38" /tissue_type="abiotic stress treated leaf and root tissue" /lab host="pOACP38" /clone lib="potato abiotic stress cDNA library" /clone lib="potato abiotic stress cDNA library" /clone lib="potato abiotic stress cDNA library" /clone lib="potato abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 3d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed by placement at 4 C. Cold stressed at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,	Contact: R Contact: R Contact: R The Instit 9712 Medic Email: pot Clones car Seq primer 1		
8 8 8 8 8 8 8 8 8 8 8 8	5 B & B &	8 8 8 8 8 8 8 8 8 8	ORIGIN Query M Best Lo Matches Qy Db Db
709 CCGATTY 709 CCGATTY 707 CTGATGA 707 CTGATGA 769 CAGCTTY 767 TAGCTTY 829 TGATCAA 829 TGATCAA 827 TGATCAA 827 TGATCAA 837 ATTGGCT 949 TCCACG			UGIN Query Match Best Local Similar: Matches 555; Con 109 ATCCACC 169 CTGTCAC 167 CTCTCAC

2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the CDNA library. RNA sample."

ORIGIN	12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."
Query Match Best Local S Matches 555	y Match 27.9%; Score 358.2; DB 14; Length 989; Local Similarity 62.9%; Pred. No. 1.3e-42; hes 555; Conservative 0; Mismatches 328; Indels 0; Gaps 0;
B &	109 ATCCACCGTTCACGTTAAGCGATCTGAAGAAAGCGATTCCTACCCATTGCTTTGAGCGAT 168
Qy	
Db 1	167 CTCTCATCCGCTCATTCTCCTATGTTGTGTATGACCTCATACTCGTCTCCATCATCTACT 226
Qy 2	229 ACCTTGCAAACACGTATATCCCTTATTCCTACACCTCTGGCTTACCTAGCATGGCCCG 288
Db 2	227 ACGTTGCAAACACTTACTTCCACCTCCTTCCATCCCCATATTGCTACATTGCGTGGCCTA 286
Ş	289 TTTACTGGTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTG 348
Db 2	287 TTTACTGGATTTGCCAGGGTTGTGTTTGCACTGGTGTTTGGGTTAATGCCCACGAATGTG 346
Qy 3	349 GTCACCATGCATTTAGCGACTACCAGTTGATGATGACATTGTTGGATTCGTGCTCCATT 408
Db 3	347 GCCATCACGCTTTCAGTGATTACCAATGGGTTGATGACACCGTTGGACTTATCCTTCACT 406
Qy 4	409 CGGCTCTCCTCACCCCGTATTTCTCTTTGGAAATATAGCCACAGGAATCACCACGCCAACA 468
Db 4	407 CTGCTCTGTTGGTGCCGTACTTCTCTTTGGAAATATAGTCATCGTCGCCACCACTCCAACA 466
Qy 4	469 CAAATTCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTCAAGATTT 528
Db 4	467 CTGGCTCCCTCGAGCGTGATGAGGTCTTTGTGCCCCAAGCCCAAAATCTCAGCTCGGATGGT 526
Qy E	529 ATTCCAAACTTCTTAACAATCCACCCGGGGGAGTGTTCACTTTGGTTTTCGGTTGACTT 588
Db 5	27
Qy 5	589 TAGGATTTCCGTTATACCTCTAACTATATCTCGGGCAAGAAATACGGGAGGTTTGCCCA 648
рь s	87
Qy 6	549 ACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTTGCTAT 708
Db 6	47
Qy 7	709 CCGATTTCGCTCTTCTCCCCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAAAAGGGG 768
Db 7	707 CTGATGCTGGAGTTCTCGGAGTTTGTTATCTGCTATACCGTGTTGCCTTAGTGAAAGGTC 766
Qy 7	69
Db 7	767 TAGCTTGGCTAGTGTGCATCTACGGTGTACCCCTCCTTGTCGTGAACGGCTTCCTTGTCC 826
Qy e	829 TGATCACATATTTGCACCACACCCCATCTCTCTCACTCCCTCATTATGATTCAACCGAATGGA 888
9b e	827 TGATCACCTACTTGCAGCACACTCACCCATCATTGCCTCACTACGATTCAACCGAGTGGG 886
Qy B	89
Db 8	87
9	949 TCCACGACGTTACACACTCACGTCTTGCATCATTTGATCTC 991
Db 9	47

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Submitted (25-APR-2002) Maize Mapping
Missouri, Columbia, MO 65211, USA
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/db_xref="MaizeDB:634972"
/db_xref="taxon:4577"
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Contact: Singh, J.A.
Eastern Cereal and Oilseed Research
Agriculture and Agri-food Canada
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1 (bases 1 to 1080)

Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Singh, P., Couroux, P., De Moors, A., Harris, L.J., Singh, P., Couroux, P., De Moors, A., Harris, L.J., Singh, P., Couroux, P., De Moors, A., Harris, L.J., Singh, P., Couroux, P., De Moors, A., Harris, L.J., P., Couroux, P.
                                                                                                                                                                                                                                        Descurainia sophia

Descurainia sophia

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BU238570 1080 bp mRNA linear EST 06-SE D801_13f05_A D801_AAFC_ECORC_cold_stressed_Flixweed_seedlings Descurainia sophia cDNA clone D801_13f05, mRNA sequence.
                                                                                          Unpublišhed (2001)
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                                                                                                                           TTACACACACTCACGTCTTGCATCATTTGATCTCATACATTCCACATTATCATGCAAAGG 1017
                                                                                                                                                                                  GGGGAGCTATGGCTACCGTAGACAGAGACTATGGAATCCTGAACAAGGTGTTTCCACAACA
                                                                                                                                                                                                                            AAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTTCCTGAATCGGGTTTTCCACGACG 957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (613) 759-1662
(613) 759-1701
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 200C/16 hrs Tight/day (average 8 leaves, 1 cm tall, weight 0.029/plant). Then they were exposed to 20C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="D801_13f05"
/tissue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Ds01_AAFC_ECORC_cold_stressed_Flixweed_seedlin
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/mol_type="mRNA"
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Pred. No. 1.6
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
Other_ESTs: EST709015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
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EST709014 potato abiotic stress cDNA library
Clone POABJ33 5' end, mRNA sequence.
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Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: potato-array@tigr.org
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               following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 °C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 °C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed aroots were harvested at 6 hr, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the CDNA library. RNA sample."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI
/note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 2
C for 3-4 weeks. Abiotic stress conditions were applied
four separate sets of plants. Set 1 involved saturation
the soil with 150 mM NaCl and tissues were harvested at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="abiotic stress treated leaf and lab_host="DH10B-TonA"
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Pred. No. 2.8e-41;
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Best Local Similarity
Matches 528; Conserv
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Solanum tuberosum (potato)

Solanum tuberosum
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: potato-array@tigr.org
Clones can be requested from TI
Seq primer: ATT TAG GTG ACA CTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 918)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B
Generation of ESTs from abiotic stressed potato tissue
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Other_ESTs: EST715109
     GTCACCATGCATTTAGCGACTACCAGTTGATTGATGACATTGTTGGATTCGTGCTCCATT
                                                      TTTACTGGATTTGCCAGGGTTGTGTTTGCACTGGTATTTTGGGTTAATGCCCACGAATGTG
                                                                                                                                                          ACGTTGCAAACACTTACTTCCACCTCCTTCCATCCCCATATTGCTACATTGCGTGGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               four separate sets of plants. Set I involved saturation of the soil with 150 mM Nacl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 20 and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 20 and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 20 and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 20 and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 20 and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 20 and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 20 and 4d and 4d
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//clone lib="potato abiotic stress cDNA library"
/clone lib="potato abiotic stress cDNA library"
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/clone lib="potato abiotic stress conditions were applied to C for 3-4 weeks. Abiotic stress conditions were applied to C for 3-4 weeks. Abiotic stress conditions were applied to C for 3-4 weeks.
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/mol_type="mRNA"
/cultivar="Kennebec"
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clone="POACK42"
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Pred. No. 3e-40;
0; Mismatches 3
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                                                                                                                                                                            Unpublished (2003)
Other ESTS: EST716262
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                               EST716261 potato abiotic stress cDNA library Solanum clone POACR59 5' end, mRNA sequence. CK270183
                                                                                                                   Email: potato-array@tigr.org
Clones can be requested from TIGR via
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 963)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue
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                                                         /organism="Solanum tuberoвum"
/mol_type="mRNA"
/cultivar="Kennebec"
/tissue_type="abiotic stress treated
/lab_host="DH10B-TonA"
                            /db_xref="taxon:4113"
/clone="POACR59"
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/clone_lib="potato abiotic stress cDNA library"
/note="vector: pCMVSport6.1; Site_1: RcoRI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."
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Query Match Best Local Similarity Matches 540; Conserv 975 543 615 603 483 855 423 795 363 735 303 675 243 183 555 123 495 435 375 63 w TIGATIGATGATGTIGGATTCGTGCTCCATTCGGCTCTCCTCACCCCGTATTTCTCT TTGCATCATTTGATCTCCATACATTTATCATGCAAAGGAAGCAAGGGATGCAATC GGGCGAGTGTTTCACTTTGGTGTTTCGGTTGACTTTTAGGATTTCCGTTATACCTCTTAACT GTGCACCATCTGTTCTCAACCATGCCACACTACAACGCGATGGAGGCAACCAAAGCAGTC TGTGACAGAGACTATGGGGTTCTAAACAAGGTCTTCCACAACATCACCGACACTCACGTG CTCTCACTCCCTCATTATGATTCAACCGAATGGAACTGGATCAAAGGCGCCTTATCAACA GTACCCCTCCTCGTCGTGAACGGCT ATTCCAGTACTAGGTGTAAGCGTGTTCTTCGTTTTGATCACATATTTGCACCACACCCAT TATGCAATCAAGCTTCTTGTAGCAGCAAAAGGGGCAGCTTGGGTAATCAACATGTACGCA TACAACAACCGTGAGAGGCTACAGATCTTCGTTTCTGATGCTGGAGTTCTCGGAGTTTGT TTCAACGATCGTGAACGCGTTCAAGTTTTGCTATCCGATTTCGGTCTTCTCGCTGTATTT AATGTATCTGGCAGACCATACGACCGATTTGCATGTCACTATGACCCTTACGGCCCAATC AATATCTCGGGCAAGAAATACGGGAGGTTTGCCCAACCACTTTGATCCCATGAGTCCAATT TTTGTGCCCAAGCCAAAATCTCAGCTCGGATGGTATTCCAAGTACTTGAACAATCCACCA TACATTCCTAAACGTAAGTCGAAGGTCAAGATTTATTCCAAACTTCTTAACAATCCACCC TGGAAATATAGTCATCGTCGCCACCACTCCAACACTGGCTCCCTCGAGCGTGATGAGGTC TGGAAATATAGCCACAGGAATCACCACGCCAACACAAATTCACTCGATAACGATGAAGTT TGGGTTGATGACACCGTTGGACTTATCCTTCACTCTGCTCTGTTGGTGCCCGTACTTCTCT CCATCATTGCCACACTACGATTCAACCGAGTGGGATTGGCTTAGGGGAGCTTTGGCAACC TATCTGCTATACCGTATTGCCTTAGTGAAAGGTCTAGCTTGGCTAGTGTGCATCTACGGT Conservative 26.2%; 0, Score 336.6; DB 14; Pred. No. 1.7e-39; 0; Mismatches 339; Indels Length 0, Gaps 1034 602 674 122 662 794 614 182 554 974 542 914 482 854 422 242 62 362 734

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ACCESSION
VERSION
KEYWORDS
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SEO6f08.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE
Gm-c1027-1504 5' similar to SW:FD62 SOYEN P48631 OMEGA-6 FATTY
DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further ir
call: (800)-533-4453 or contact via email: ccu@resgen.com
Insert Length: 1297 Std Error: 0.00
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 286 1800
314 286 1810
/clone lib="Gm-c1027"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhOI; This cDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old Williams seedlings
which were propagated on paper towels with distilled
water. The cotyledons were flash-frozen in liquid
mitrogen, then lyophilized for 72 hours. Unequal amounts
of mRNA was used for cDNA synthesis. Stratagene's cDNA
Synthexix Kit (catalog number 200401) was used to
synthesize the cDNA. First- stranded synthesis was
                                                                                                                                                                                                                                                                                                     /tissue_type="cotyledons seedlings"
                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-1504"
                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Glycine max"
                                                                                                                                                                                                                                                                                 lab host="DH10B"
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/STEMS CLONE ID:
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performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3' end of the primer (AGAGAGAGAGAGAGAGAGAGAGAGTAGTCTGGAG(T)18] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the CDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript(tm) II XR predigested vector (pBluescript II SX(+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserte, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia

ORIGIN

S Ś 밁 Ś 밁 S Ś 밁 5 ş 밁 5 밁 Ś 맑 밁 5 밁 밁 밁 밁 Query Match
Best Local Similarity
Matches 484; Conserv 834 438 378 654 318 594 534 618 498 774 258 198 474 138 414 354 CATGCATTTAGCGACTACCAGTTGATTGATTGATTGTTGGATTCGTGCTCCATTCGGCT 294 18 78 TTCGGTCTTCTCGCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAAAAGGGGCAGCT ATCAAAGGCGCCTTATCAACAATCGATAGGGATTTCGGGTTTCCTGAATCGGGTTTTCCAC ACATATTTGCACCACACCCATCTCTCACTCCCTCATTATGATTCAACCGAATGGAACTGG CTCCTCACCCCGTATTTCTCTTGGAAATATAGCCACAGGAATCACCACGCCAACACAAAT CATGCATTCAGTGACTACCAGTTGCTTGATGATATTGTTGGCCTTGTCCTCCACTCCGGT TGGGCTGTCCAAGGTTGCATCCTTACTGGAGTTTGGGTCATTGCCCATGAGTGTGGCCAC TTGAGAGGAGNCTTAGCAACAGTGGATAGAGATTATGGGATNCTGAAACAGGTCTTNNCA ACATTCTTGCAGCATACTCACCCTGCATTGNCACATTACACTTCCTCTGAGTGGGACTGG TGNGTGGTGTGTTTATGGAGTTCCATTGCTAGTGGTCAATGGATTTTTGGTGTTGATT TGGGTAATCAACATGTACGCAATTCCAGTACTAGGTGTAAGCGTGTTCTTCGTTTTGATC GCAGGAGTACTTGCAGTATGCTATGGCCTTTTCCGTCTTGCCATGGCAAAAGGACTTGCC TTTGATCCCATGAGTCCAATTTTCAACGATCGTGAACGCGTTCAAGTTTTGCTATCCGAT TGGCCCTTGTACTTGGCTNTAAATGTTTCTGGAAGGCCTTATGATAGATTTGCTTGCCAC TTTCCGTTATACCTCTTAACTAATATCTCGGGCAAGAAATACGGGAGGTTTGCCAACCAC ANACTTCTTANCANTCCACCCGGGGGAGTGTTCACTTTGGTGTTTCGGTTGACTTTAGGA TCACTCGATAACGATGAAGTTTACATTCCTAAACGTAAGTCGAAGGTCAAGATTTATTCC CTCCTAGTCCCATACTTTTCATGGAAATACAGCCATCGCCGTCACCACTCCAACACTGGT TGGTTTTGTCAAGCTAGCATCCTCACCGGCCTCTGGGTCATCGGTCACGAATGTGGTCAC AAATACCTTAACAATCCTCCAGGCAGAGTCCTCACTCTTGCTGTCACCCTCACACTTGGT TCTCTTGAGCGGGATGAAGTATTTGTGCCAAAGCAGAAGTCCTGTATCAAGTGGTACTCT Conservative 25.9**%**; 64.9**%**; Score 332.2; DB 1 Pred. No. 8.6e-39; 0; Mismatches 262 DB 10; 262; Indels ٥, Gaps 413 137 833 497 773 437 713 377 653 317 593 257 533 677 893 557 197 77 617

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GACGTTACACACACTCACGTCTTGCATCATTTGATCTCATACATTCCACATTATCATGCA 101:

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386 CATTGTTGGATTCGTGCTCCATTCGGCTCTCCTCACCCCCGTATTTCTCTCTTGGAAATATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seg primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
Other_ESTs: EST725062
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Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
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32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."
                                                                                                                                                                                                                                                                                                                                                           for 3-4 weeks. Abiotic stress conditions were applied four separate sets of plants. Set 1 involved saturation the soil with 150 mM wacl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:hhr, 6hr, 12hr, and 2d) set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested aft cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clome lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site 1: EcoR1; Site 2: Not1;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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                                                          Score 330.4; DB 14;
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0; Mismatches 336;
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Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 616)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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Unpublished (2002)
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belongs to contig QH_CA_Contig3889, see http://cgpdb.uc
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/note="Vector: pBRcDNASfiAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_SEQ=Not found"
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cultivar="RHA801"
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lone="QHI14E14"
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Pred. No. 2e-38;
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121
                                                                                                                                                                                                    390 GTTGGATTCGTGCTCCATTCGGCTCTCCTCACCCCGTATTTCTCTTGGAAATATAGCCAC 449
                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616,
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyle rosids; Vitaceae; Vitis.
1 (bases 1 to 831)
Goes da Silva,F., Iandolino,A., Lim,H.,
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                            AAGTCGAAGGTCAAGATTTATTCCAAACTTCTTAACAATCCACCCGGGCGAGTGTTCACT 569
ANATOCANACTOGGATGGTACTOCANATACOTGANCANTOCACTTGGTCGATTCGTCACA
                                                                                  CGCCGCCATCATTCTAATACCGGTTCCCTCGAGAAGGATGAAGTCTTTGTCCCCAAAAACC
                                                                                                                          AGGAATCACCACGCCAACACAAATTCACTCGATAACGATGAAGTTTACATTCCTAAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer: GCCAAACGAATGGTCTAG
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Bud; Vector: pDNR; Site_1: Sfir; Site_2: Sfir; CABUD is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5'and 3' adaptors were used in cloning as follows:
5'-ANGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and 5'-ATTCTAGAGGCCGGGCGCACATTACGGCCGGG-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."
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/cultivar="Cabernet Sauvignon
/db_xref="taxon:29760"
/clone="CAbud0002_IIIR_E01"
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Pred. No. 1.8e-38;
0; Mismatches 277;
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1170 ATGTAATCA 1178 	1110 TGCATCTACATCGAGCCCGATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAG	1050 GAGTACTATAAAATCGACAGGACTCCAATTTTCAAAGCAATGTATAGAGAGGCTAAGGAA	990 TCATACATTCCACATTATCATGCAAAGGAAGGCAAGGGATGCAATCAAGCCAGTGTTGGGC	930 GGGTTCCTGAATCGGGTTTTCCACGACGTCTACACACTCACGTCTTGCATCATTTGATC	870 TÄTGATTCAACCGAATGGAACTGGATCAAAGGCGCCTTATCAACAATGGATAGGGATTTC	810 GTAAGCGTGTTCTTCGTTTTGATCACATATTTGCACCCACACCCCATCTCTCACTCCCTCAT	750 CTTGTAGCAGCAAAAGGGGCAGCTTGGGTAATCAACATGTACGCAATTCCAGTACTAGGT	690 CGCGTTCAAGTTTTGCTATCCGATTTCGGTCTTCTCGCTGTATTTTATGCAATCAAGCTT	630 AAATACGGGAGGTTTGCCAACCACTTTGATCCCATGAGTCCAATTTTCAACGATCGTGAA	570 TIGGTGTTTCGGTTGACTTTAGGATTTCCGTTATACCTCTTAACTAATATCTCGGGCAAG
	AAAGGTGTGTTCTGGTACCACAAG 1169 AAAGGTGTTTTCTGGTACCAGAAT 777	GCAATGTATAGAGAGGCTAAGGAA 1109 GAATGTGAAGAGAGGCAAAGGAG 720	GATGCAATCAAGCCAGTGTTGGGC 1049 NAGGCCATAAAGCCAGTATTAGGA 660	ACTCACGTCTTGCATCATTTGATC 989	TTATCAACAATCGATAGGGATTTC 929	CACACCCATCTCTCACTCCCTCAT 869	ATGTACGCAATTCCAGTACTAGGT 809	GCTGTATTTTATGCAATCAAGCTT 749	AGTCCAATTTTCAACGATCGTGAA 689 	CTCTTAACTAATATCTCGGGCAAG 629
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Sequence

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EWN	241 KGAAWVINMYAIPVLGVSVEFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLN 300	179 FTLGFPLYLFTNISGKKYERFANHFDPMSPIFKERERFQVLLSDLGLLAVLYGVKLAVAA 238	181 LTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAA 240	119 LHSFLMTPYFSWKYSHRNHHANTNSLDNDEVYIPKSKAKVALYYKVLNHPPGRLLIMFIT 178	121 LHSALLTEYFSWKYSHRNHHANTNSLDNDEVYIFKRKSKVKIYSKLLNNPPGRVFTLVFR 180	59 FYFLADKYIPILPAPLAYLAWPLYWFCQASILTGLWVIGHECGHHAFSDYQWVDDTVGFI 118	61 FYYLANTYIPLIFTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFV 120	1 MGGGGRGRTSQKPLMERVSVDPPFTVSDLKQAIPPHCFKRSVIRSSYYIVHDAIIAYI 58	ERVPVDPPFT	Query Match 79.9%; Score 1636; DB 4; Length 375; Best Local Similarity 76.9%; Pred. No. 1.1e-164; Matches 289; Conservative 40; Mismatches 45; Indels 2; Gaps 1;	ORGANISM: Crepis alpina 09-161-994A-2	LENGTH: 375	EQ ID NO 2	SEQ ID NOS: 26	FILING DATE: 1996-03	PARTITION NUMBER: 9801236 4	APPLICATION NO	REFERENCE: BAFOR=1	CANT: LENMAN, Marit	STYMNE,	APPLICANI: LEE, MICHAEL APPLICANT: SJODAL, Staffan	••	DAHLQVIST	APPLICANI: BAROK, MAUTONI	L INFORMATION:	nce 2, Application US/09161994A : No. 6333448	994A

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RESULT 2
US-09-059-769-4
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                                                                                                            Query Match
Best Local Similarity
                                                                                                  Matches 286;
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                                                                                                                                                                                                                                                              TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                 TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: AU PO6226 FILING DATE: 15-APR-1997 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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IIILE OF INVENTION: Therefor
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SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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60 VFYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGF 119
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                                                   MGAGGRMSDPSEGKNILERVPVDP-PFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAY 59
                                MGAGGR--GRTSEKSVMERVSVDPVTFSLSDLKQAIPPHCFQRSVIRSSYYVVQDLIIAY 58
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Singh, Surinder
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SYSTEM: PC-DOS/MS-DOS
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75.7%;
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                                                                                              ; Score 1598.5; DB; Pred. No. 1e-160; 41; Mismatches 4
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                                                                                                                               DB 4;
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US-09-059-769-2
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                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
SEQUENCE CHARACTERISTICS: LENGTH: 374 amino acid
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CORRESPONDENCE ADDRESS:
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                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                               NAME: Ferber, Donna M. REGISTRATION NUMBER: 3
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APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 61
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
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FILING DATE: APPLI 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06223
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APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
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TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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5370 Manhattan Circle, Suite 201
                                                                                                                                                                                             US 60/050403
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; TYPE: amino a ; TOPOLOGY: lir ; MOLECULE TYPE: US-09-059-769-2
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US-08-872-302-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08872302
Patent No. 5846784
GEMERAL INFORMATION:
APPLICANT: Hitz, William D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
               TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R
REGISTRATION UNMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                        ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Fatty Acid Modifying Enzymes From TITLE OF INVENTION: Developing Seeds of Vernonia galar NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: E.I. o
STREET: 1007 Mark
CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                     STATE: Delaware
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||| ||: |||:|||: 374
IEP--DSKLKGVYWYHKL 374
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384 amino acids
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                                                                                                  BB-1084
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Pred. No. 9e-160;
40; Mismatches 4
                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
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US-09-638-937-15
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-302-4
                                                                                                                                                                                       ; ORGANISM: Borago officinalis US-09-638-937-15
                                                                                                                                                                                                                            NUMBER MICE
SOFTWARE: MICE
SEQ ID NO 15
FRIGTH: 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6593514
GENERAL INFORMATION:
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                                                                                                                            Matches
                                                                                                                                      Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cahoon, Edgar B
APPLICANT: Hitz, William D
APPLICANT: Ripp, Kevin G
APPLICANT: Ripp, Kevin G
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF CALENDIC ACID, AN UNUSUAL
TITLE OF INVENTION: FATTY ACID CONTAINING DELTA-8,10,12 CONJUGATED DOUBLE
TITLE OF INVENTION: BONDS
                                                                                                                                                                                                                                                                             FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/638,937
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: BB-1371-P1
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                      TYPE: PRT
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6593514
MGGGGRMPVPTKGKKSKSDVFQRVPSEKPPFTVGDLKKVIPPHCFQRSVLHSFSYVVYDL 60
                                                                             MGAGGRMSDPSEGK----NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
                                                                                                                                                                                                                                                                   Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAAKGAAWVINMYA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHHLISYIPHYHAKBARDAIKPVLGBYYKIDRTPIFKAMYRBAKBCIYIBPDEDSEHKGV
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                                                                                                                           Conservative
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                                                                                                                         68.2%; Score 1396.5; DB 4 63.9%; Pred. No. 2.6e-139; rative 62; Mismatches 70;
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76.5%;
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Pred. No. 1.4e-158;
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                                                                                                                                                      DB 4;
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RESULT 6
US-09-059-769-12
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                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Green, A
APPLICANT: Singh, S
APPLICANT: Lenman,
APPLICANT: Stymne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IERAL INFORMATION:
IERAL INFORMATION:
IPPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/059
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
FILING DATE: 15-APR-1997
                                                                                                                                                                        FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                              FILING DATE: 16-APR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Col
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CITY: E
TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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FILE REFERENCE: BAFOR=1
CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 383
TYPE: PRT
ORGANISM: Glycine max
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US-09-161-994A-16
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Best Local Similarity 61.2
Matches 232; Conservative
                                                                               Query Match 65.9%;
Best Local Similarity 61.2%;
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                                                                 Matches
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                   APPLICANT: LENMAN, MARIT
TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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ORIGINAL SOURCE:
ORGANISM: Sol
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o. 6333448
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                 1 MGAGGRMSDPS----BGKNILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVYDL
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ECLYVEKDESSQGKGVFWY 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAFOR,
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STYMNE, Sten
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                                                                   Conservative
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; Pred. No. 3.1e-134; 
65; Mismatches 77; Indels 5;
                                                                   65;
                                                                 Score 1348.5; DB 4;
Pred. No. 3.1e-134;
5; Mismatches 77;
                                                                   Indels
                                                                                                Length 383;
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RESULT 8
US-09-059-769-11
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                                                                                             PILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043
PILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,7
PILING DATE: APX11 14, 1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: AU PO6223
PILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6226
PRIOR APPLICATION NUMBER: AU PO6226
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TELEFAX: (303)
INFORMATION FOR SEQ
                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses
NIVER OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Circle, Suite 201
          ELECURAL: (303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                 499-8089
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                                                                                                                                                                                     US 60/050403
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RESULT 9
US-09-161-994A-15
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                                                                                                                      CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 383
Query Match
Best Local Similarity
Matches 233; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09161994A
Patent No. 6333448
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 233; Conservative
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Best Local Similarity 61.3%; Pred. No. 8.4e-132;
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                   APPLICANT: LEE, Michael
APPLICANT: SJODAL, Staffan
APPLICANT: STYMNE, Stein
APPLICANT: LENMAN, Marit
TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
FILE REFERENCE: BAFOR-1
                                                                                       TYPE: PRT
ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                           GUMMESON, Per-Olov
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DAHLQVIST, Anders
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                64.8%;
; Score 1325.5; DB 4;
; Pred. No. 8.4e-132;
62; Mismatches 80;
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                                 Length 383;
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Conservative

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RESULT 10
US-08-675-650B-2
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                                                                                                       ; MOLECULE TYPE:
US-08-675-650B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08675650B Patent No. 5850026
GENERAL INFORMATION:
APPLICANT: DeBonte, L. et al.
       Matches
                                                     Query Match
                                                                                                                                                                                                                                                  TELEFAX: 612/288-9696
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compo
OPERATING SYSTEM: PC-
SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,650B
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 60 South a
                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    NAME: Lundquist, Ronald C. REGISTRATION NUMBER: 37,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-JUL-1996
CLASSIFICATION: 800
                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                     TELEPHONE:
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VENTION: CANOLA OIL HAVING INCREASED OLEIC ACID

VENTION: DECREASED LINOLENIC ACID CONTENT
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          Conservative
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  64.4%; Score 1318; DB 2; 61.2%; Pred. No. 5.2e-131; tive 61; Mismatches 81;
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                                                     Length 384;
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       Gaps
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CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 384
TYPE: PRT
ORGANISM: Brassica napus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES
FILE REFERENCE: 07148-063002
                                                                                                                                                                         121
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Pred. No. 5.2e-131;
1; Mismatches 81;
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APPLICANT: Kodali, Dharma
APPLICANT: Kodali, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
TITLE OF INVENTION: PATTY ACID CONTENT
FILE REFERENCE: 07148-072001
CURRENT APPLICATION NUMBER: US/09/128,602B
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOPTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 384
TYPE: PAT
ORGANISM: Brassica napus
US-09-128-602B-14
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US-09-128-602B-14
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Sequence 14, Application US/09995297
Patent No. 6649782
GENERAL INFORMATION:
APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
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GENERAL INFORMATION:

APPLICANT: DeBonte, Lorin R.

APPLICANT: Shorrosh, Basil S.

ITITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEF

TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEF

TITLE REFERENCE: 07148-063002

CURRENT APPLICATION NUMBER: US/09/354,231B

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 08/874,109

PRIOR APPLICATION NUMBER: US 08/874,109

PRIOR APPLICATION NUMBER: US 08/874,109

SOPTWARE: FASTE OF SEQ ID NOS: 69

SOPTWARE: FASTESQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 384

TYPE: PRT
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US-09-354-231B-10
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; TYPB: PRT
; ORGANISM: Brassica napus
US-09-995-297-14
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US-09-354-231B-10
Query Match
Best Local Similarity
Matches 234; Conserv
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Best Local Similarity
Matches 233; Conserv
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    Conservative
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  64.3%; Score 1317; DB 4;
61.3%; Pred. No. 6.7e-131;
tive 58; Mismatches 82;
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    Indels
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RESULT 15
US-09-133-962A-4
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GENERAL INFORMATION:
                                                                                       TELEX: 835420
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JONATHAN EDWARD LIGHTNER
JOHN JOSEPH OKULEY
TITLE OF INVENTION: GENES FOR MICROSOMAL
DELTA-12 DESATURASES
ENZYMES FROM PLANTS
MOLECULE
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BB-1043-D TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRV 174
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/133,962A FILING DATE: 14-Aug-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09133962A
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                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGAGGRM-----SDPSEGKNILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHD
                                                                                                                                                          TELEPHONE: (302)992-5481
TELEFAX: (302)773-0164
                                                                                                                                                                                                                                                    NAME: CHRISTENBURY, LYNNE M. REGISTRATION NUMBER: 30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19898
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                                                                   LENGTH: 384 amino acids
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AND RELATED
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-133-962A-4
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Best Local Similarity 61.3
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           1 MGAGGRM-----SDPSEGKNILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHD 54
                                                                                                                                                                                                                                                                                                                                                          1 MGAGGRMQVSPPSKKSETDNI-KRVPCETPPFTVGELKKAIPPHCFKRSIPRSFSYLIWD 59
                                                                                                                                                                                                                                                              DIVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRV 174
                                                                             RDFGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYRE 353
                                                        RDYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPVVKAMWRE 359
                                                                                                                 FTLVFRLTLGFPLYLLTNISGKKY-GRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYA 233
                     AKECIYIEPDEDSEHKGVFWYH 375
                                                                                                                                                                           VMLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYG
AKECIYVEPDROGEKKGVFWYN
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Pred. No. 6.7e-131;
SB; Mismatches 82;
381
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299 293 239

Search completed: June Job time : 24 secs 18, 2004, 17:39:02

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Post-processing: Minimum Match 0%
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[ Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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1 MGAGGRMSDPSEGKNILERV.....IYIEPDEDSEHKGVFWYHKM 377
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TA	14 1310	13 1318	12 1318	11 1323.5	10 1325.5	_	8 1346.5		6 1356.5	5 1356.5		3 1589.5	2 1592	1 1633.5	Result No. Score
64.3	64.4	64.4	64.4	64.7	64.8	65.1	65.8	65.9	66.3	66.3	68.2	77.7	77.8	79.8	Query Match
384	384	384	384	383	383	383	392	383	395	383	383	374	373	384	Query Match Length DB
9	16	10	9	9	ø	9	12	ø	12	12	12	9	9	9	DB.
US-09-995-297-10	US-10-715-100-14	US-09-771-904-14	US-09-995-297-14	US-09-852-399-4	US-09-837-751-31	US-09-837-751-6	US-10-425-114-56017	US-09-981-124-12	US-10-425-114-40643	US-10-424-599-266787	US-10-464-631-15	US-09-981-124-2	US-09-981-124-4	US-09-981-124-20	ID
Semience 10 April	Sequence 14, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 4, Appli	Sequence 31, Appl	Sequence 6, Appli	Sequence 56017, A	Sequence 12, Appl	Sequence 40643, A	Sequence 266787,	Sequence 15, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 20, Appl	Description

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1 MGAGGRMSDPSEG-KNILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVA 58

44.	44	43	42	41	40	39	38	37	36	35	34	u u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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63.3	יי ני	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.6	63.8	63.8	63.8	64.0	64.0	64.0	64.0	64.0	64.0	64.1	64.1	64.1	64.1	64.1	64.1	64.1	64.2	64.3	64.3
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14	٥	16	15	10	9	9	9	9	9	9	16	10	9	16	10	9	16	10	9	16	15	10	9	16	10	9	15	16	10
US-10-060-793-48	115-09-837-751-4	US-10-715-100-2	US-10-435-521-2	US-09-771-904-2	US-09-995-297-2	US-09-981-124-9	US-09-885-189-6	US-09-885-188-6	US-09-837-751-32	US-09-981-124-10	US-10-715-100-8	US-09-771-904-8	US-09-995-297-8	US-10-715-100-18	US-09-771-904-18	US-09-995-297-18	US-10-715-100-16	US-09-771-904-16	US-09-995-297-16	US-10-715-100-6	US-10-435-521-6	US-09-771-904-6	US-09-995-297-6	US-10-715-100-12	US-09-771-904-12	US-09-995-297-12	US-10-330-775-4	US-10-715-100-10	US-09-771-904-10
Sequence 48, Appl	4	Sequence 2, Appli	Sequence 2, Appli	e 2	2	Sequence 9, Appli	6	6	•	9	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl		e 16,	16,	6	ς,	-	Sequence 6, Appli	H	e 12,	12,	Sequence 4, Appli	10,	Sequence 10, Appl

ALIGNMENTS

RESULT 1 US-09-981-124-20

GENERAL INFORMATION:

Sequence 20, Application US/09981124 Patent No. US20020166144A1

```
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Singh, Surinder
APPLICANT: Lennan, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
TITLE OF INVENTION: FATTY ACID METABOLISM
PILE REFERENCE: 26-98A
CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILLING DATE: 2001-10-17
PRIOR PILLING DATE: 2001-10-17
PRIOR PILLING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILLING DATE: 1997-04-15
PRIOR PILLING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR PILLING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR PILLING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 384
TYPE: PRT
US-09-981-124-20
Ouery Match
Patch 79.8%; Score 1633.5; DB 9; Length 384;
Best Local Similarity 82.7%; Pred. No. 2.3e-158;
Matches 296; Conservative 28; Mismatches 31; Indels 3; Gaps 3;
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PRIOR FILLING DATE: 1998-04-10-1, PRIOR FILLING DATE: 1998-04-14
PRIOR FILLING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILLING DATE: 1997-04-16
PRIOR FILLING DATE: 1997-04-15
PRIOR FILLING DATE: 1997-04-15
PRIOR PILLING DATE: 1997-04-15
PRIOR PILLING DATE: 1997-04-15
PRIOR PILLING DATE: 1997-04-15
PRIOR PILLING DATE: 1997-06-20
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                                                                                                                                                                                                        ; NAME/KEY: misc_feature

; LOCATION: (937)...(937)

; OTHER INFORMATION: N is any nucleotide residue

; NAME/KEY: misc_feature

; LOCATION: (901)...(901)

; OTHER INFORMATION: N is any nucleotide residue

US-09-981-124-4
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US-09-981-124-4
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                                                                                                    Query Match
Best Local S
Matches 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
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TITLE OF INVENTION: PATTY ACID EPOXYGENASE
TITLE OF INVENTION: PATTY ACID METABOLISM
FILE REFERENCE: 26-98A
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LOCATION: (292)...(292)
OTHER INFORMATION: The 'Xaa'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                             MGAGGRMSDFSEGKNILERVFVDF-FFTLSDLKKAIFTHCFERSVIRSSYYVVHDLIVAY 59
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MGAGGR--GRSE-KSVMERVSVDPVTFSLSDLKQAIPPHCFQRSVIRSSYYVVQDLIIAY 57
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                                                                                                    77.8%; llarity 75.9%; Conservative 40
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                                                                                                    Score 1592; DB 9; Length 373;
Pred. No. 4e-154;
0; Mismatches 45; Indels
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CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR PILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR PILING DATE: 1997-04-15
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US-09-981-124-2
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; SEQ ID NO 2
FUNCTH: 374
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Patent No. US20020166144A1
                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 285; Conserv
                                                                                                                                                                                                                                                                                                                                                                     Query Match
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TITLE OF INVENTION: FATTY ACID BPOXYGENASE
TITLE OF INVENTION: FATTY ACID METABOLISM
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APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
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SOFTWARE: PatentIn version
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TYPE: PRT
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                           238 NKGAAWVACMYGVPVLGVFTFFDVITFLHHTHQSSPHYDSTEWNWIRGALSAIDXDFGFL
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                                                                                                      60 VFYYLANTYIPTLIFTPLAYLAMPVYMFCQASILTGLMVIGHECGHHAFSDYQLIDDIVGF 119
59 IFYPLANTYIPTLFTSLAYLAMPVYMFCQASVLTGLMVIGHECGHHAFSNYTWFDDTVGF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn version 3.1
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                                                                                                                                                                                                             MGAGGR--GRTSEKSVMERVSVDPVTFSLSELKQAIPPHCFQRSVIRSSYYVVQDLIIAY 58
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  ILHSFLLTPYFSWKFSHRNHHSNTSSIDNDEVYIPKSKSKLARIYKLLNNPPGRLLVLII 178
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                                                                                                                                                                                                                                                                                                                 77.7%; Score 1589.5; DB 9; llarity 75.4%; Pred. No. 7.3e-154; Conservative 40; Mismatches 48;
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CURRENT APPLICATION NUMBER: US/10/464,631
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US/09/638,937
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: BB-1371-P1
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 383
TYPE: PRT
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US-10-464-631-15
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Best Local Similarity
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APPLICANT: Hitz, William D
APPLICANT: Ripp, Kevin G
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF CALENDIC ACID, AN UNUSUAL
TITLE OF INVENTION: FATTY ACID CONTAINING DELTA-8,10,12 CONJUGATED DOUBLE
TITLE OF INVENTION: BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Borago officinalis
                     356
                                                         301
                                                                                                                                                      236 LLVAAKGAAWVINMYAIPVLGVSVEFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRD 295
                                                                                                                                                                                                         181 VLLVQLTLGWPLYLMFNVSGRPYDRFACHFDPKSPIYNDRERLQIYISDAGIVAVMYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242;
ECIYIEPDEDSEHKGVFWY
                                                                           FGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK 355
                                                                                                                                                                                                                                   TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK 235
                                                                                                                                                                                                                                                                                      TVGLLLHSALLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKRSGISWSSEYLNNPPGRVL
                                                                                                                                                                                                                                                                                                          IVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVF 175
                                                                                                                                                                                                                                                                                                                                                               VIAALFFYTASRYIHLQPHPLSYVAWPLYWFCQGSVLTGVWVIAHECGHHAFSDYQWLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGAGGRMSDPSEGK----NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL 55
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                                                         YGFLNKVLHNITDTHVAHHLFSTMPHYHAMBATKAIKPILGDYYQCDRTPVFKAMYREVK
                                                                                                                                  RLVAAKGVAWVVCYYGVPLLVVNGFLVLITYLQHTQPSLPHYDSSEWDWLKGALATVDRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.2%; Score 1396.5; DB 1; 63.9%; Pred. No. 4.3e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Mismatches
                     374
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RESULT 5
US-10-424-599-266787
; Sequence 266787, Application US
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Sequence 40643, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 266787
LENGTH: 383
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Best Local :
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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APPLICANT: Kovalic David
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ORGANISM: Glycine
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              FGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIAFCLYYVATHYFHLLÞSÞLSFLAWÞIYWAVQGCILTGVWVIAHECGHHAFSDYQLLDD
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                                                                                                                                                                                                                                                                                                                      ECIYVEPDOSTESKGVFWYN 380
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Pred. No. 5.4e-130;
Mismatches 77;
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40643
LENGTH: 395
TYPE: PRT
ORGANISM: Glycine max
FEATURE: TRECEMBRICAN COLUMBER TRECEMBRICAN COLUMBER TO THE TRECEMBRICAN COLUMBER TO T
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US-09-981-124-12
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US-10-425-114-40643
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION UNMBER: US 09/059769
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
SEQ ID NO 12
LENGTH: 383
TYPE: PRT
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Best Local Similarity 62.4
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID SPOXYGENASE
TITLE OF INVENTION: FATTY ACID METABOLISM
FILE REFERENCE: 26-98A
                                                                              PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
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APPLICANT: Singh, Surinder
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; Pred. No. 5.6e-130;
61; Mismatches 77; II
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US-09-981-124-12
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SEQ ID NO 56017
LENGTH: 392
                                                                                                                                                                                                                                             Matches 236;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine FEATURE:
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; OTHER INFORMATION: Clone ID: 701211444_FLI.pep US-10-425-114-56017
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APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28
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70 TIAFCLYYVATHYFHLLPSPLSFLAWPIYWAVQGCILTGVWVIAHECGHHAFSDYQLLDD
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                                                                                                             1 MGAGGRMSDPSEGK----NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
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                                                                                       MCAGGRTDVPPANRKSEVDPLKRVPFEKPPFSLSQIKKVIPPHCFQRSVFRSFSYVVYDL
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Pred. No. 3.6e-129;
55; Mismatches 77;
                                                                                                                                                                                 Score 1346.5; DB 1
Pred. No. 5.9e-129;
1; Mismatches 78;
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APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Liu, Qing
ITILE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
FILE REFERENCE: 45-00
CURRENT APPLICATION NUMBER: US/09/837,751
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,124
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 383
TYPE: PRT
ORGANISM: Gossypium sp.
US-09-837-751-6
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US-09-837-751-6
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                                                                                                                                                                                                                                                                                                                                                          Query Match
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nes 230; Conserv
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                                         FGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK 355
                                                                         RIVLAKGVGWVISVYGVPLLVVNAFLVMITYLQHTHPSLPHYDSSEWDWMRGALSTVDRD
                                                                                      LLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRD 295
                                                                                                                          SITIQLTLGWPLYLAFNVAGRPYDRFACHYDPYGPIFSDRERLQIYISDAGVLAVAYALY 240
                                                                                                                                        TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK 235
                                                                                                                                                                            TVGLILHSSLLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKKSGLRWWAKHFNNPPGRFL
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ECIYIEPDEDSEHKGVFWY 374
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60.7%; Pred. No. 1.5e-127;
7ative 70; Mismatches 74;
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GENERAL INFORMATION:

APPLICANT: Qiu, Xiao
ITILE OF INVENTION: PRODUCTION OF CONJUGATED LINOLEIC AND
ITILE OF INVENTION: LINOLENIC ACIDS IN PLANTS
IFILE REFERENCE: BNZ-002
CURRENT APPLICATION NUMBER: US/09/852,399
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: USSN 60/203,027
PRIOR FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ for Windows Version 4.0
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US-09-837-751-31
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US-09-852-399-4
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LENGTH: 383
TYPE: PRT
                                                                                                                                                                                                                                                       Sequence 4, Application US/09852399 Patent No. US20020045232A1
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Best Local Similarity 61.3%;
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CURRENT APPLICATION NUMBER: US/09/837,751
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,124
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
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APPLICANT: Singh, Surinder
APPLICANT: Liu, Qing
TITLE OF INVENTION: Method of Modifying the Content of Cottonseed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK 235
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Pred. No. 8e-127;
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                                                                                                                                                                        SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 14
LENGTH: 384
TYPE: PRT
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: Forn, Zhegong
APPLICANT: PLANTS, SEEDS AND OILS HAVING
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING
TITLE OF INVENTION: PATTY ACID CONTENT
FILE REFERENCE: 07148-072002
CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
CURRENT FILING DATE: 2001-11-27
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LENGTH: 383
TYPE: PRT
ORGANISM: Calendula officinalis
                                                                                                               Query Match
Best Local Similarity
Matches 233; Conserv
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PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
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IIASCFYYVATTYFPLLPHPLSYFAWPLYWACQGCVLTGVWVIAHECGHHAFSDYQWLDD
             | IVAYVEYYLANTYIPLIPTPLAYLAMPVYMFCQASILTGLMVIGHECGHHAFSDYQLIDD 115
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                                                                                                               64.4%; Score 1318; DB 9;
61.2%; Pred. No. 4.7e-126;
tive 61; Mismatches 81;
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US-09-771-904-14
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                                          DFGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGBYYKIDRTPIFKAMYREA
                                                                                     FRYAAAQGVASMVCFYGVPLLIVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDR
                                                                                                     KLLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDR
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                         DYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPVVKAMWREA
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Pan, Zhegong
APPLICANT: Miao, Guo-Hua
APPLICANT: Miao, Guo-Hua
FITIE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THER
FILE REFERENCE: 07148-063003
CURRENT APPLICATION NUMBER: US/09/771,904
CURRENT FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 384
TYPE: PRI
ORGANISM: Brassica napus
US-09-771-904-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09771904 Publication No. US20030131379A1
                                                                                    Query Match 64.4%; Score 1318; DB 10; Best Local Similarity 61.2%; Pred. No. 4.7e-126; Matches 233; Conservative 61; Mismatches 81;
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KECIYVEPDRQGEKKGVFWYN 381

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RESULT 15
US-09-995-297-10
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; TYPE: PRT
; ORGANISM: Brassica
US-10-715-100-14
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US-10-715-100-14
                                                                                                                                                                                                                           Sequence 10, Application US/09995297 Patent No. US20020092038A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.4%; Score 1318; DB 16; Best Local Similarity 61.2%; Pred. No. 4.7e-126; Matches 233; Conservative 61; Mismatches 81;
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TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED TITLE OF INVENTION: PATTY ACID CONTENT

FILE REPERENCE: 07148-072002

CURRENT APPLICATION NUMBER: US/10/715,100

CURRENT FILING DATE: 2003-11-17

PRIOR APPLICATION NUMBER: US/09/995,297

PRIOR FILING DATE: 2001-11-27

PRIOR FILING DATE: 1998-08-03

NUMBER: OF SEC ID NOS: 68

NUMBER: OF SEC ID NOS: 68
                    APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
TITLE OF INVENTION: FATTY ACID CONTENT
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APPLICANT: Fan, Z
APPLICANT: DeBont
REFERENCE: 07148-072002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEMNWIKGALSTIDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYGILNKVFHNITDTHVAHHLFSTMPHYHAMBATKAIKPILGEYYQFDGTPVVKAMWREA
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; ORGANISM: Brassica
US-09-995-297-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.3%;
Best Local Similarity 61.3%;
Matches 234; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
 360
                                                     300
                                                                                                        180
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                                                                                                                                                                                                                                 115 DIVGFVLHSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRV 174
                          354
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                                                                                                                                                                                       175 FTLVERLTLGFPLYLLTNISGKKY-GRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYA 233
                                                                                                                                                                                                                                                                       60 IIIASCEYYVATTYFPLLEHPLSYFAWPLWACQGCVLTGVWVIAHECGHHAFSDYQWLD
                                                                                                                                                                                                                                                                                   384
                                                     RDFGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGBYYKIDRTPIFKAMYRE
AKECIYVEPDRQGEKKGVFWYN
                                                                                                                                                                                                                   DTVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKKSDIKWYGKYLNNPLGRT
                         AKECIYIEPDEDSEHKGVFWYH 375
                                                                                                                                                               VMLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYG
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                                                                                                                                                                                                                                                                                                                                                                             Score 1317; DB 9;
Pred. No. 6e-126;
8; Mismatches 82;
  381
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119

59

4.

Search completed: June Job time: 49 secs 18, 2004, 17:43:53

> 359 353

293

239

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
June 18, 2004, 17:34:22; Search time 20 Seconds (without alignments)
105-10-069-772-2
Perfect score: 2047
Sequence:
1 MGAGGRMSDPSEGKNILERV......IYIEPDEDSEHKGVFWYHKM 377
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

: PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	8	Query	Length	BB	ID	cription
–	1348.5	65.9	383	2	T10480	Delta12 fatty acid
N	w	65.3	382	N	T15042	fatty
w	1332.5	65.1	383	N	T10789	6 desati
4	•	64.8	383	N	T07688	σ
տ	•		385	N	T09880	σ
σ	•	62.2	387	N	T09839	
7	٠		383	N	T15043	
œ	1237.5		387	N	T07687	σ
9	1220	59.6	378	N	T14269	N
10	1160.5	٠	333	N	T07009	fatty
11	926.5	•	376	N	JC7871	yl-CoA
12	658.5	•	359	N	AG2005	fatty
13	653	•	359	N	S52650	3 fatty
14	645	31.5	441	N	T03029	-3 fatty
15	639.5	•	460	N	T10063	3 fatty
16	w	•	381	N	T03923	le omega
17	627	•	431	N	T07685	ω +
18	620.5	•	386	μ	JQ2335	-3 fatty
19	612	٠	379	N	JC2555	3 fatty
20	607	٠	398	N	T01696	-3 fatty
21	607	•	404	N	PQ0812	-3 fatty
22	606	•	418	N	JC7872	yl-CoA
23	606	29.6	446	μ	JQ2336	fatty a
24	604.5	•	443	N	T01697	3 fatty
25	602.5	٠	453	_	JQ2339	3 fatty
26	593.5	29.0	380	N	T10898	Ė
27	593	•	438	N	T15039	3 fatty
28	590.5	٠	377	_	JQ2337	omega-3 fatty acid
,	1	,				

RESULT 2

	292	-	301		306		316.5			339				585	
10.5	14.3	14.3	14.7	14.9	14.9	15.1	15.5	15.6	16.1	16.6	16.6	20.9	28.0	28.6	28.7
352	351	443	448	424	349	351	447	347	424	350	350	376	380	380	383
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	-
B69901	S54259	T08136	D85362	T07742	\$43770	S11519	853309	843771	JC5891	AH2005	843772	T26075	JQ2338	T06235	A44227
fatty-acid desatur	Deltal2 fatty acid	probable omega-6 d	hypothetical prote	omega-6 desaturase	phosphatidylcholin	phosphatidylcholin	n-6 fatty acid des	phosphatidylcholin	omega 6 desaturase	phosphatidylcholin	phosphatidylcholin	hypothetical prote	omega-3 fatty acid	omega-3 fatty acid	omega-3 fatty acid

ALIGNMENTS

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망	Ş	B 전	D _D	8	Дb	Ş	Db	Ş	뮹	Q	Db	\$	Query Ma Best Loo Matches	RESULT 1 T10480 Delta12 fatty C;Species: Sol C;Accession: T R;Consiglio, F submitted to t A;Reference nu A;Accession: T A;Molecule typ A;Residues: 1- A;Cross refere A;Experimental C;Superfamily: Ox
361 ECLYVEKDESSQGKGVFWY 379	356 ECIYIEPDEDSEHKGVFWY 374	296 FGFLNKVEHDVIHTHVLHHLLSYIPH HAKEAKDAIKKVLGEYYKIDKIFIFKAMYKEAK 		236 LLVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRD	181 SLTITLTLGWPLYLAFNVSGRPYDRFACHYDPYGPIYNNRERLQIFISDAGVLGVCYLLY	PLYLLTNISGKKYGRFANHFDPMSPIFN	121 TVGLILHSALLVPYFSWKYSHRRHHSNTGSLERDEVFVPKPKSQLGWYSKYLMNPPGRVL	NTNSLDNDEV	61 ILVSIMYYVÄNTYFHILIPSPYCYIAWPIYWICQGCVCTGIWVNÄHECGHHÄFSDYQWVDD	56 IVAYVEYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDD		1 MGAGGRMSDPSEGKNILERVPVD-PPFTLSDLKKAIPTHCPERSVIRSSYYVVHDL	atch 65.9%; Score 1348.5; DB 2; cal Similarity 61.2%; Pred. No. 1.6e-105; 232; Conservative 65; Mismatches 77; I	tty acid desaturase (EC 1.14.99) [imported] Solanum commersonii (Commerson's wild potato) -701.1999 #sequence_revision 16-Jul-1999 #text n: T10480 c, F.; Amatruda, M.R.; Leone, A.; Costa, A.; G to the EMBL Data Library, November 1995 e number: Z17044 n: T10480 preliminary; translated from GB/EMBL/DDBJ type: mRNA : 1-383 <con> ferences: EMBL:X92847; NID:g1054842; PID:g1054 ntal source: clone ScDes D111 ily: omega-3 fatty acid desaturase : oxidoreductase; unsaturated fatty acid biosy</con>
				TEWNWIKGALSTIDRD 295	FISDAGVLGVCYLLY 240	VLLSDFGLLAVFYAIK 235	LGWYSKYLNNPPGRVL 180	VKIYSKLLNNPPGRVF 175	HECGHHAFSDYQWVDD 120	HECGHHAFSDYQLIDD 115	FQRSLIRSFSYVVYDL 60	FERSVIRSSYYVVHDL 55	Length 383; Indels 5; Gaps 2;	- Commerson's wild potato)) t_change 09-Jun-2000 Grillo, S. Grillo, S.

```
T15042
omega-6 fatty acid desaturase (EC 1.14.99.-) - parsley
cyspecies: Petroselinum crispum (parsley)
cybate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
cyaccession: T15042
R;Kirsch, C:; Hahlbrock, K:; Somssich, I.E.
Plant Physiol. 115, 283-289, 1997
A;Title: Rapid and transient induction of a parsley microsomal of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second comparison of the second com
                                                                                                                                                                                                                                      R;Liu, Q.; Singh, S.P.; Green, A.; Sharp, P.J.; Marshall, D.R. submitted to the EMBL Data Library, March 1999
A;Description: Isolation and characterisation of two different A;Reference number: Z17145
A;Accession: T10789
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                      omega-6 desaturase, microsomal - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
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A;Cross-references: EMBL:U86072; NID:g2501789; C;Superfamily: omega-3 fatty acid desaturase
                                                                                                                                                      A;Cross-references: EMBL:Y10112
A;Experimental source: subspeci
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A; Residues: 1-383 <LIU>
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    65.1%; Score 1332.5; DB 2 60.7%; Pred. No. 3.4e-104; tive 70; Mismatches 74;
70;
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Pred. No. 1.7e-104;
9; Mismatches 74;
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(;Species: Glycine max (soybean)
(;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
(;Accession: T07688
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
Plant Physiol. 110, 311-319, 1996
A;Reference number: Z16095; MUID:96151506; PMID:8587990
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: involved in production of polyunsaturated lipids A;Note: constitutively expressed in both vegetative tissues and C;Superfamily: omega-3 fatty acid desaturase
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A; Residues: 1-383 <HEP>
A; Cross-references: EMB
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C;Function:
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R;Liu, Q.
submitted to the EMBL Data Library,
A;Reference number: Z16895
A;Accession: T09880
A;Accession: T09880
A;Status: preliminary; translated f:
A;Molecule type: mRNA
A;Residues: 1-385 <LIU>
RESULT 6
T09839
cleate 12-hydroxylase - castor bean
C;Species: Ricinus communis (castor bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
C;Accession: T09839
R; van de Loo, F.J.; Broun, P.; Turner, S.; Somerville, C.R.
Proc. Natl. Acad. Sci. U.S.A. 92, 6743-6747, 1995
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A; Experimental source: cultivar
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C;Species: Gossypium hirsutum (upland cotton)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000

C;Accession: T09880
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Similarity 59.6%; Pred. No. 3.6e-101;
27; Conservative 61; Mismatches 86;
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                                                                                                                                                                                                            GVLNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGKYYPFDGTPIYKAMWREAKE
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fungal elicitor-induced protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-20
C;Accession: T15043
R;Kirsch, C; Hahlbrock, K; Somssich, I.E.
Plant Physiol. 115, 283-289, 1997
A;Title: Rapid and transient induction of a parsley microsomal delta 12 if
A;Reference number: Z18274; MUID:97451781; PMID:9306702
A;Accession: T15043
A;Accession: T15043
A;Accession: T15043
A;Molecule type: mRNA
A;Residues: 1-383 <KIR>
A;Cross-references: EMBL:U86374; NID:g2501791; PIDN:AAB80697.1; PID:g2501
C;Genetics:
A;Gene: ELI12
C;Superfamily: omega-3 fatty acid desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: An oleate 12-hydroxylase from Ricinus communis L. is a fatty acyl A;Reference number: Z16877; MUID:95350145; PMID:7624314
Ä;Accéssión: T09839
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-387 <DEL>
A;Cross-references: EMBL:UZ2378; NID:g722350; PIDN:AAC49010.1; PID:g722351
A;Experimental source: strain Baker 296; tissue-type developing endosperm
C;Superfamily: omega-3 fatty acid desaturase
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                                                                                 MGAGGRMSDPSEGK----NILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
MGAGGRMSDPPSGKKTAAEALKRAPHEKPPFTIGDLKKAIPAHCFQKSLVTSFRYLIQDL
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                                                                                                                                           60.6%;
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                                                                                                                                           Score 1241.5; DB Pred. No. 1.5e-96;
                                                                                                                              Mismatches
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omega-6 desaturase FAD2-1, microsomal - soybean
(;Species: Glycine max (soybean)
(;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
(;Accession: T07687
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
R;Heppard, E.P.; Miao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: involved in production of polyunsaturated lipids; A;Note: strongly expressed in developing seeds C;Superfamily: omega-3 fatty acid desaturase
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C;Function:
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A;Experimental source:
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                                                                   LNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAKECI
                                                                                                                                                                                                                        VILIIGWPMYLAFNVSGRPYDSFASHYHPYAPIYSNRERLLIYVSDVALFSVTYSLYRVA
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                       LNKVFHHITDTHVAHHLFSTMPHYHAMEATNAIKPILGEYYQFDDTPFYKALWREARECL
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                                                                                             C;Accession: T07009
R;Gadea, J.; Mayda, E.; Conejero, V.; Vera, P.
Mol. Plant Microbe Interact. 9, 409-415, 1996
A;Title: Characterization of defense-related genes ecto
A;Reference number: Z15859; MUID:96252900; PMID:8672818
                                                                                                                                                                                                                   omega-6 fatty acid desaturase (EC 1.14.99.-) defense-related - C;Species: Lycopersicon esculentum (tomato) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: desaturates oleic acid to linoleic acid C;Superfamily: omega-3 fatty acid desaturase C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
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A; Molecule type: mRNA
A; Residues: 1-333 <GA
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                                                                   A; Reference number: A; Accession: T07009
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A;Cross-references: EMBL:U91341; NID:g2290403; PID:g2290404
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A; Accession: T14269
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A; Molecule type: mRNA
A; Residues: 1-376 <SUG>
A; Cross-references: DDBJ AB075526
C; Comment: This enzyme is involved
C; Genetics:
A; Gene: fad2
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                             C;Species: Chlorella vulgaris
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
C;Accession: JC7871
R;Suga, K.; Honjoh, K.; Furuya, N.; Shimizu, H.; Nishi, K.; Shinohara, F.; Hirabaru, R;Suga, K.; Honjoh, Biochem. 66, 1314-1327, 2002
B;Title: Two low-temperature-inducible Chlorella genes for delta12 and omega-3 fatty s cerevisiae, and expression of omega-3 fad in Nicotiana tabacum.
A;Reference number: JC7871; MUID:22152188; PMID:12162554
A;Accession: JC7871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stearoyl-CoA 9-desaturase (EC 1.14.19.1), FAD2 - Chlorella vulgaris
N;Alternate names: acyl-CoA desaturase; delta12 stearoyl-CoA desaturase; delta9-desatura
C;Species: Chlorella vulgaris
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
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A;Experimental sourc
C;Genetics:
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Best Local :
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                                                                                                                                                                  Similarity
LVW-ASTFIDAAPVPAAVRWLALWPAYWYLAGAVATGIWVIAHECGHQAFSDYQAVNDGV
                          FYYLANTYIPLIPTPLA--YLA-WPVYWFCQASILTGLWVIGHBCGHHAFSDYQLIDDIV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECIYIEPDEDSEHKGVFWY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGFLNRVFHDVTHTHVLHHLISYIPHYHAKBARDAIKPVLGEYYKIDRTPIFKAMYRBAK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLVFRLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVGFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGAGGRM----SDPSEGKNILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDL
                                                                      ATTRAPSAEG---WTRQPVNTKPAFSVSTLRKAIPAHCWQRSLPRSCAYLAADLLALAA
                                                                                                AGGRMSDPSEGKNILERVPVD--PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVTLTQGLAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECIFVEKDKD---KGVYWY 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGLLNKVFHNVTDTHVLHHIFSYISHYHAMEAKKAIKPLLGEYYKYDDTPILKAMWRDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGGGGNMSAMTSKNEQKKNPLERVPSSKPPFTLGDVKKAIPPHCFERSLVKSFSFLIQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVGLILHSALLTPYFAWKHSHRRHHANTGSLENDEIYIPRLKSKLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVAYVFYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nces: EMBL:X94944; NID:g1161567; PIDN:CAA64414.1; PID:g1161568 source: cultivar Rutgers; leaf
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                             is involved
                                                                                                                                                                  45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.7%; Score 1160.5; D
55.1%; Pred. No. 8e-90;
tive 54; Mismatches
                                                                                                                                                76;
                                                                                                                                            Score 926.5; DB 2;
Pred. No. 4.1e-70;
/6; Mismatches 117;
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                                                                                                                                                                                                                                                                             ij.
                                                                                                                                                                                                                                                                         low temperature adaptation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIVLITLMHHTHSSLPHYDSSEWDHLRGALATVDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                              Indels
                                                                                                                                                                                Length 376;
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                                                                                                                                                                                                                                                                         and is also involved
                                                                                                                                              Gaps
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omega-3 fatty acid desaturase [imported] - Nostoc sp. (strain PCC 7120)
()Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG2005
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000019; PIDN:BAB77963.1; PID:g17135417; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: C;Genetics: A;Gene: all1597 C;Superfamily: omega-3 fatty acid desaturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary A;Molecule type: DNA
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Best Local
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hes 121; Conserv
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                                                                                                                                                                                                                                                                                                                                              77
                                                                                                                                                                                                                                                                                                                                                                                                                                24
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  LKATEAIKPVMGEYYRKSEEPIWKSLWRSCVSCHFV-PD
                                                                                                                                                                                                                                                          NIDNDESWYPVTQSQYK-----EMPLGQKIGRYYVFLLAYPVYLFKRSPNKE----GSH
                                                                                                                                                                                                                                                                                                                                          WLIQGTWFWALFVVGHDCGHQSFSKHKWLNDLIGHLTHTFILVPYHGWRISHRTHHKNTG 136
                                                                                                                                                                                                                                                                                                                                                                                  WFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFVLHSALLTPYFSWKYSHRNHHANTN 144
                                          KEARDAIKPVLGEYYKIDRTPIFKAMYREAKECIYIEPD 363
                                                                                    TFLHHTEADLPWYRGEDWTFLKGAISSIDRNYGLVNHIHHDI-GTHVAHHIFLNIPHYNL 305
                                                                                                                 TYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLNRVFHDVTHTHVLHHLISYIPHYHA 324
                                                                                                                                                                      FLPSSSLFKPSEKWDVITSTVLWSCMVGLLGFLTYQWGWMWLLKYYAAPYIVFVIWLDLV
                                                                                                                                                                                                           FDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAAKGAAWVINMYAIPVLGVSVFFVLI 264
                                                                                                                                                                                                                                                                                                  SLDNDEVYIPKRKSKVKIYSKLLNNPPGRVFTLVFRLTLGFPLYLLTNISGKKYGRFANH 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAYVFYYLANTYIPLIPTPLAYLAWPVY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCRYVAPDTPGD--GVLWFRK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAASFGWAMLVKTWLVPYLVVNFWLVTITMLQHSHPELPHYGEDEWDWLRGALTTVDRDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLVLHSLLLVPYYSWKHSHRRHHSNTGNVVKDEVFVPPTREEVSDKWELEQAWPIRLVKL
                                                                                                                                                                                                                                                                                                                                                                                                                              PFTLODLKAAIPAECFQPNVSKSLFYFFRDVLIVGLLYAVAH-YLD-----SWYFWPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GF-LARVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FITLTLGWPLYLAFNVASRPYEKSWVNHFDPWSPIFSKRELVEVAVSDAALVAVLCGLRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVAAKGAAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.2%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76; Mismatches 123;
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Pred. No. 1.2e-47;
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343
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, M.; Yasuda, M.; Tabata, S
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RESULT

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A,Cross-references: GB:D13780; NID:g600596; PIDN:BAA02924.1; PID:g600598 A,Note: the authors translated the initiation codon GTG for residue 1 as R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y. o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yanda, Res. 3, 109-136, 1996
                   omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common tobacco (;Species: Nicotiana tabacum (common tobacco) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000 C;Accession: T03029 R;Hamada, T.; Nishiuchi, T.; Kodama, H.; Nishimura, M.; Iba, K. Plant Cell Physiol. 37, 606-611, 1996 A;Title: CDNA cloning of a wounding-inducible gene encoding a plastid omega-3 A;Reference number: Z14828; MUID:96416425; PMID:8819308
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A;Residues: 1-359 «KAN»
A;Cross-references: EMBL:D90913;
A;Note: the nucleotide sequence w
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Variety: PCC 6803
C; Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 20-Jun-2000 C; Accession: S52650; S75843
R; Sakamoto, T.; Los, D.A.; Higashi, S.; Wada, H.; Nishida, I.; Ohmori, M.; Plant Mol. Biol. 26, 249-263, 1994
A; Title: Cloning of omega-3 desaturase from cyanobacteria and its use in al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: delta
C;Species: Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 omega-3 fatty acid desaturase (EC 1.14.99.-) - Synechocystis sp.
N.Alternate names: delta 15 desaturase
A; Reference number: A; Accession: T03029
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A; Residues: 1-359 < SAK>
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                                                                                                                                                                                                                                                                                                                SYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAKECIYIEPDEDSEHKGVFW 373
                                                                                                                                                                                                                                                                                                                                                             FVVWLDLVTFLHHTEDNIPWYRGDDWYFLKGALSTIDRDYGFINPIHHDI-GTHVAHHIF
                                                                                                                                                                                                                                                                                                                                                                                 VSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLNRVFHDVTHTHVLHHLI 316
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3.5e-47;
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da, M.; Yas
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A;Gene: FAD7
C;Superfamily
C;Keywords: o
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A;Molecule type: mRNA
A;Residues: 1-441 <HAN's
A;Cross-references: EMBL:D79979; NID:g1694624; PIDN:BAA11475.1; PID:g1694625
A;Experimental source: cultivar SR1
C;Genetics:
                                                                                                                                                                           C;Function:
A;Pathway: fatty acid biosynthesis
C;Superfamily: omega-3 fatty acid
                                                                                                                                                                                                                                                                                                                                           A,Title: Plasmid omega-3 fatty acid desaturase cDNA from A,Reference number: Z16930; MUID:94302177; PMID:8029360 A,Accession: T10063
                                                                                                                                                                                                                                                                                                                                                                                                                                      omega-3 fatty acid desaturase (EC 1.14.99.-)
N;Alternate names: linoleoyl desaturase
C;Species: Ricinus communis (castor bean)
C;Date: 16-U11-1999 #sequence_revision 16-U1
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                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-460 < DEL>
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Plant Physiol. 1
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VIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFVLHSALLT
                               DFGFLNRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYK 340
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105, 443-444, 1994
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72; Mismatches
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Search Job ti	B 8	§ §	Ş	Db	ğ	ФФ	ş	gg	ş	용
Search completed: June 18, 2004, 17:38:26 Job time : 21 secs	436 VSDTGDVVYYQK 447	377 I-GTHVIHHLFPQIPHYHLVEATEAAKPVMGKYYREPKKSGPLPLHLLGSLVRSMKEDHY 435	306 VTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAKECIY 359	317 KLYGIPYWIFVMWLDFVTYLHHHGHEDKLPWYRGKAWSYLRGGLTTLDRDYGWINNIHHD 376	248 NMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLNRVFHD 305	261 YLWSRSPGKKGSHFHPDSGLFVPKERKDIITSTACWTAMAALLVYLNFSMGFVQML 316		205 PYHGWRISHRTHHQNHGHVENDESWHPLSEKIFKSLDNVTKTLRFSLPFPM-LAYPF 260	128 PYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVFTLVFRLTLGFPL 187	155WVAWPLYWFCQGTMFWALFVLGHDCGHGSFSNNPKLNSVVGHLLHSSILV 204

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OM protein - protein search, using sw model

Run on: June 18, 2004, 17:30:33 ; Search time 18 Seconds (without alignments) 1090.580 Million cell updates/sec

Title: Perfect score: Sequence: US-10-069-772-2
2047
1 MGAGGRMSDPSEGKNILERV.....IYIEPDEDSEHKGVFWYHKM 377

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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32	94	4.6	313	_	CCSA_TOBAC	
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ALIGNMENTS

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EMBL; Y16285; CAA76158.2; InterPro; IPR005804; FA_desat Pfam; PF00487; FA_desaturase; ProDom; PD001081; FA_desat fa Oxidoreductase; Fatty acid bi TRANSMEM 77 97 TRANSMEM 77 97 TRANSMEM 110 130 TRANSMEM 172 132 TRANSMEM 172 192 TRANSMEM 218 238 TRANSMEM 218 238 TRANSMEM 242 262 DOMAIN 98 102	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinfor the European Bioinformatics Institute. use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).	-I- COFACTOR: Ir -I- PATHWAY: POI -I- SUBCELLULAR -I- TISSUE SPECI -I- DOMAIN: The and/or be in -I- SIMILARITY:	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Lee M., Lenman M., Banas A., Nilsson R., Liljenberg C., I Green A., Stymne S.; "Identification of non-heme and epoxy group formation.", Science 280:915-918(1998). -i- FUNCTION: Changes the de triple bond in the biosy -i- CATALYTIC ACTIVITY: Linc	1 12 CRAL 81931; 8-FEB-200 8-FEB-200 8-FEB-200 8-FEB-200 9-FEB-200 1-FEB-200 9-FEB-200 1-FEB-200
1 FA	s SWISS-PROT entry is copyright. It is ween the Swiss Institute of Bioinformatics Institute. The Swiss Profit institutions as long by non-profit institutions as long lified and this statement is not removed ities requires a license agreement (See lities requires to license@isb-sib.ch).	COPACTOR: Iron. COPACTOR: Polyunsaturated fatty acid biosynthesis PATHWAY: Polyunsaturated fatty acid biosynthesis SUBCELULAR LOCATION: Integral membrane protein TISSUE SPECIFICITY: Seed. DOMAIN: The histidine box domains may contain the DOMAIN: The histidine box domains may contain the and/or be involved in metal ion binding. SIMILARITY: Belongs to the fatty acid desaturase	ENCE FROM N.A. INE=98239771; PubMed=9572738; M., Lenman M., Banas A., Bafor M., Singh S., income R., Liljenberg C., Dahlqvist A., Gummeson R., Stymme S.; Intification of non-heme diiron proteins that empoxy group formation."; Inco 280:915-918(1998). FUNCTION: Changes the delta-12 double bond of triple bond in the biosynthesis of crepenynic CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2)	REAL STANDARD; PRT; 375 AA. 31; 31; 328-2003 (Rel. 41, Created) 328-2003 (Rel. 41, Last sequence update) 328-2003 (Rel. 41, Last annotation update) 329-2003 (Rel. 41, Last sequence (EC 1.14, 329-329-329-329-329-329-329-329-329-329-
76158.2; 104; FA desat famdesat_desat; 1FA desat fam; 2. atty acid biosynt 74 POTEN 97 POTEN 130 POTEN 130 POTEN 238 POTEN 238 POTEN 102 HISTI	ntry is copyri s Institute of nformatics Ins it institutio statement is a license agr	R: Iron. : Polyunsaturated fatty acid biosynthesis. : Polyunsaturated fatty acid biosynthesis. !!! Polyunsaturated fatty acid biosynthesis. !!! Polyunsaturated fatty acid desaturase !!! Iry: Belongs to the fatty acid desaturase !!!	PubMed=9572738; Banas A., Bafo nberg C., Dahlqv S.; f non-heme diiro ormation."; 18(1998). 1998). The delta-1 n the biosynthes	RD; PRT; Created) Last sequence, Last annotate, dehydrogenase fatty acid ace itae; Streptopl itophyta; eudi
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                  RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;

RY "Developmental and growth temperature regulation of two different microsomal omega-6 desaturase genes in soybeans.";

RI microsomal omega-6 desaturase genes in soybeans.";

RL Plant Physiol. 110:311-319(1996).

CC -!- FUNCTION: ER (microsomal) omega-6 fatty acid desaturase introduces continued to the second double bond in the biosynthesis of 18:3 fatty acids, conjugate to constituents of plant membranes. It is thought to use conjugate to generate to phosphatidylcholine and to act on fatty acids conjugate to phosphatidide.

CC -- Esterified to phosphatidylcholine and, possibly, other phospholipids.

CC -- PATHMAY: Polyunsaturated fatty acid biosynthesis.

CC -- SUBCELLULAR LOCATION: Endoplasmic retriculum.

CC -- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.

CC -- SIMILARITY: Belongs to the fatty acid desaturase family.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Omega-6 fatty acid desaturase, endoplasmic re
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RESULT 3

FD6E BRAJU

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PRT; 384 AA.

AC Q39287;

DT 15-UUL-1998 (Rel. 36, Created)

DT 15-UUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-6 fatty acid desaturase, endoplasmic reticulum (BC 1.14.19.-)

DE (Delta-12 desaturase).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microsomal omega-6 desaturase.";
(In) Plant Gene Register PGR95-1
-!- FUNCTION: ER (microsomal) om
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. 651-2-5-7-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     esterified to phosphatidylcholine and, possibly, other phospholipids (By similarity).

PATHWAY: Polyunsaturated fatty acid biosynthesis.
SUBCELLULAR LOCATION: Endoplasmic reticulum.

DOMAIN: The histidine box domains may contain the active and/or be involved in metal ion binding.

SIMILARITY: Belongs to the fatty acid desaturase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial tries requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ER (microsomal) omega-6 fatty acid desaturase introduce the second double bond in the biosynthesis of 18:3 fatty acids, important constituents of plant membranes. It is thought to use cytochrome b5 as an electron donor and to act on fatty acids
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RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Wincker P., Cotione N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Bangert S.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Rooner P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
Cole Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta B.,
RA Monifort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F. X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Riazo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Riazo M., Maltis R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Militscher J., Sahamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Watchabe A., Yamada M., Yasuda M., Tabatau S.,
RA Watchabe A., Wada Zh., Marki N., Shinpo S., Takeuchi C., Wada T.,
RA Watchabe A., Wada
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Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 PJ
and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okuley J., Lightner J., Feldmann K.A., Yadav N., Lark E., Brows "Arablidopsis FAD2 gene encodes the enzyme that is essential for polyunsaturated lipid synthesis."; Plant Cell 6:147-158(1994).
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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01-NOV-1995 (Rel.
28-FEB-2003 (Rel.
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MEDLINE=94176997; PubMed=7907506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
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 (Rel. 33, Created)
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-I- FUNCTION: ER (microsomal) omega-6 fatty acid d
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Pfam; PF00487; FA_desaturase;
ProDom; PD001081; FA_desat_fam
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-!- TISSUE SPECIFICITY: Strongly expressed in developing see
-!- DOMAIN: The histidine box domains may contain the active and/or be involved in metal ion binding.
-!- SIMILARITY: Belongs to the fatty acid desaturase family.
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FADD-1.

GlyCine max (Soybean).

GlyCine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane.
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                                                                                         FVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVFTLV
                                                                                                                                                   YVFYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVG
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VTLTIGWPMYLAFNVSGRPYDSFASHYHPYAPIYSNRERLLIYVSDVALFSVTYSLYRVA
                                                           LTLHSTLLVPYFSWKISHRRHHSNTGSLDRDEVFVPKPKSKVAWFSKYLNNPLGRAVSLL
                                                                                                                          FIF-YIATTYFHLLPQPFSLIAWPIYMVLQGCLLTGVMVIAHECGHHAFSKYQMVDDVVG
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HISTIDINE BOX-2.
HISTIDINE BOX-3.
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Pred. No. 2.6e-92;
D; Mismatches 90;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Delta-12 fatty acid desaturase (EC 1.14.99.-).
Mortierella isabellina (Umbelopsis isabellina).
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Mucorales incertae sedis; Umbelopsis.
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HISTIDINE BOX-2.
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                                         use by modified
                                                                                                                                                                                                                                                                  Liu L., Li M., Xing L., Hu G.;
"Delta 12 fatty acid desturase gene of Mortierella alpina.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
to linoleic acid (delta9, delta12-18:2).
-!- PARTHWAY: C20 polyunsaturated fatty acid biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
-!- SIMILARITY: Belongs to the fatty acid desaturase family.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Delta-12 fatty acid desaturase (EC 1.14.99..)
Mortierella alpina.
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakuradani E., Kobayashi M., Ashikari T., Shimizu S.; "Identification of deltal2-fatty acid desaturase from arachidonic acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing Morticrella fungus by heterologous expression in the acid-producing fungus by heterologous expression in the acid-producing fungus by heterologous expression in the acid-producing fungus by heterologous expression in the acid-producing fungus by heterologous expression in the acid-producing fungus by heterologous expression in the acid-producing fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression fungus by heterologous expression
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Mortierellaceae; Mortierella.
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requires a license agreement (See http://www.isb-sib.ch/announce,
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                                     institutions as long as atement is not removed. U
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send

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email to license@isb-sib.ch).

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RESULT 8
FD3C SESIN
ID CARROL STANDARD; PRT
ID CARROL SESIN
ID CARROL SESIN
P48620;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequen
DT 28-FEB-2003 (Rel. 41, Last annota
DE Omega-3 fatty acid desaturase, ch
GN FAD7.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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TRANSMEM 91
TRANSMEM 199
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EMBL; AF110509;
EMBL; AF417244;
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GO:0016021; C:integral to membrane;
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156; Conser
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                                                                                                                      VWRSFRECRFVE----DHGDVVFFKK
                                                                                                                                        MYREAKECIYIEPDEDSEHKGVFWYHK 376
                                                                                                                                                             TVDRSFGKFLDHMFHGIVHTHVAHHLFSQMPFYHAEEATYHLKKLLGEYYVYDPSPIVVA
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                                                                                                                                                                                                                                                                                           YHSWRISHSKHHKATGHMTKDQVFVPKTRSQVGLPPK--ENAAAAVQEEDMSVHLDEEAP
                                                                                                                                                                                                                                                                                                      YFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNN-------
                                                                                                                                                                                                                                                                                                                                     DKFENPLIRYLAWPAYWIMQGIVCTGIWVLAHECGHQSFSTSKTLNNTVGWILHSMLLVP
                                                                                                                                                                                                                                                                                                                                               PLIPTPL-AYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFVLHSALLTP
                                                                                                                                                                                                                                                                                                                                                                               PTSAKPAPERNYQLPEFTIKEIRECIPAHCFERSGLRGLCHVAIDLTWASLL-FLAATQI
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111 POTENTIAL.
219 POTENTIAL.
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                     Last sequence update)
Last annotation update)
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> PN (IN REF. 2).
V (IN REF. 2).
> V (IN REF. 2).
> V (IN REF. 2).
> S (IN REF. 3).
A -> VAV (IN REF. 1).
-> T (IN REF. 1).
-> I (IN REF. 1).
-> I (IN REF. 1).
+> Q (IN REF. 2).
+ 40B2FC1C1E01F93F CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 781; DB 1;
Pred. No. 1.5e-55;
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AAA - > V
AAA - > T
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HISTIDINE
HISTIDINE
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STS -> TTT
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                                                                 PRT;
           chloroplast
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BOX-2.
BOX-3.
                                                                B
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          precursor
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            (E)
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Query Match
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Matches 132; Conser
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sesamum indicum (Oriental sesame) (Gingelly).
Bukaryota; Viridiplantae; Streptophyta; Embryo.
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Lamiales; Pedaliaceae; Sesamum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD001081; FA o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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STRAIN=CV.
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FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactchlipids, sulfolipids and phosphatidylglycerol. PATHWAY: Polyunsaturated fatty acid biosynthesis.
SUBCELULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
SIMILARITY: Belongs to the fatty acid desaturase family.
  356
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DYGWINNIHHDI-GTHVIHHLFPQIPHYHLIBATBAAKPVLGKYYR
                                                                                            VI--
                                                                                                                     LVAAKGAAWVINMYAIPVLGVSVFFVLITYLHH--THLSLPHYDSTEWNWIKGALSTIDR
                                                                                                                                                                                                                                                                                                      VLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVFTLVF
                                                                                                                                                                                                                                                                                                                                                                                     VFYYLANTYIPLIPTBLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGRMSDPSEGKNILERVPVDPPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAY----
                                         DEGELNRVEHDVTHTHVLHHLISYIPHYHAKEARDAIKEVLGEYYK
                                                                                                                                                                               PL-LAYPIYLWSRSPGKQ----GSHFHPDSDLFVPNEKKDVITSTVCWTAMLALLVGLSF
                                                                                                                                                                                                                      RLTLGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDF---GLLAVFYAIKL
                                                                                                                                                                                                                                                                                                                                                           VAAYFNN---
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                                                                                                                                                                                                                                                                    ILHSSILVPYHGWRISHRTHHQNHGHVENDESWHPLSE---
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llarity 38.2%;
Conservative 6
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94; TISSUE=Cotyledon;
                                                                                       -GPVQLLKLYGIPYLGNVMWLDLVTYLHHHGHEDKLPWYRGKEWSYLRGGLTTLDR
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atty_acid_biosynthesis;
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447
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                                                                                                                                                                                                                                                                                                                                                         -WVVWPLYWFAOSTMFWALFVLGHDCGHGSFSNDPKLNSVVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
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HISTIDINE BOX-1.
HISTIDINE BOX-2.
HISTIDINE BOX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 642; DB 1;
Pred. No. 2.5e-44;
3; Mismatches 109
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hyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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RESULT 9
FD3C_RICCO

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Best Local
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01-FEB-1996
01-FEB-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Physiol. 105:443-444(1994).

- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfollipids and phosphatidylglycerol.

- PACHWAY: Polyunsaturated fatty acid biosynthesis.

- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005804; FA_desat_fam.
PfAm; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
Oxidoreductase; Fatty_acid_biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalypheae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Baker 296; TISSUE=Seed; MEDLINE=94302177; PubMed=8029360;
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricinus communis (Castor bean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van de Loo F.J., Somerville C.R.;
"Plasmid omega-3 fatty acid desaturase cDNA from Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAD7A-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T10063; T10063.
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                                                                                       128
                                                                                                                     155
                                                                                                                                               83
                                                                                                                                                                               96
                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                        EGKNILERVPVDPPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAY----VFYYLANT
                          YLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAAKGAAWVI
                                                                                 PYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVFTLVFRLTLGFPL
                                                                                                                                                                             EGKGEFFDAGAPPFTLADIRAAIPKHCWVKNPWRSMSYVLRDVVVVFGLAAVAAYFNN-
                                                        PYHGWRISHRTHHONHGHVENDESWHPLSE---KIFKSLDNVTKTLRFSLPFPM-LAYPF
                                                                                                                                               YIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFVLHSALLT 127
                                                                                                                   -----WVAWPLYWFCQGTMFWALFVLGHDCGHGSFSNNPKLNSVVGHLLHSSILV
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213
380
460 /
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                                                                                                                                                                                                                                       Conservative
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181
217
384
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35.5%;
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 -GSHFHPDSGLFVPKERKDIITSTACWTAMAALLVYLNFSMGPVQML
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annotation update
                                                                                                                                                                                                                                                                                                             CHLOROPLAST (POTENTIAL).
OMEGA-3 FATTY ACID DESATI
HISTIDINE BOX-1.
HISTIDINE BOX-2.
HISTIDINE BOX-3.
                                                                                                                                                                                                                                                     Score 639.5; DB 1
Pred. No. 4.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chloroplast
                                                                                                                                                                                                                                                                                                  836592904EF3C7B0 CRC64;
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                   DB 1;
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316
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RESULT 10
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MEDIINE-22954850; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Pa
Yamada K., Lim J., Dale J.M., Chen M., Pham
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee
                                                                                                                                                                     Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I. Fe Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Fe Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creas Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss Gierman W.C., White O., Bisen J.A., Salzberg S.L., Fras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cmega-3 fatty acid desaturase, endoplasmic re
FAD3 OR ATZGZ9980 OR FZ3F1.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FD3E AR
P48623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia; TISSUE=Hypocotyl; Watahiki M.C., Yamamoto K.T.; Submitted (SEP-1993) to the EMBL/GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94302147; PubMed=8029334;
Yadav N.S., Wierzbicki A., Aegerter M., Cast
Kinney A.J., Hitz W.D., Booth J.R. Jr., Schw
Allen S.M., Blackwell M., Reiter R.S., Carls
Feldmann K.A., Pierce J., Browse J.;
"Cloning of higher plant omega-3 fatty acid
Plant Physiol. 103:467-476(1993).
                                                                                                                                                                                                                                                                         STRAIN=cv. Columbi
MEDLINE=20083487;
                                                                                                                                                                                                                                                                                                                                   Nishiuchi T., Nishimura M., Arondel V., "Genomic nucleotide sequence of a gene fatty acid desaturase from Arabidopsis plant Physiol. 105:767-768(1994).
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
MEDLINE=94345020; PubMec
Nishiuchi T., Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                           STRAIN=cv.
                                                                                                                                 "Sequence and thaliana.";
                                                                                                                                                             Venter J.C.;
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                                                                                                                                                                                                                                                                            PubMed=10617197;
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                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376
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Schweiger B., Stecca K.I
Carlson T.J., Russell S.I
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     Lee J.M.,
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                 Palm C.J.
                                                                                                                                                                                                       Creasy T.H.,
                                                                                                                                                                           Fraser C.M.,
                                                                                                                                               Arabidopsis
                                                                                                                                                                                                                      S., Umayam
                                                                                                                                                                                                                                               Feldblyum
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                                              C.J.
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     Toriumi
                                Cheuk R.F.,
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Chao O
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC004680; AAC31854.1; -.
EMBL; AY003966; AAL36322.1; -.
EMBL; AY003462; AAM20102.1; -.
EMBL; JQ2335; JQ2335.
InterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome.";
Science 302:842-846(2003).
Science 302:842-846(2003).
In FUNCTION: Microsomal (ER) omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 18:3 fatty acids, important constituents of plant membranes. It is thought to use cytochrome b5 as an electron donor and to act on fatty acids esterified to phosphatidylcholine and, possibly, other
                                                                                                                                                                                                                                           DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F., Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamse R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L22931; AAA61778.1; -. EMBL; D17579; BAA04505.1; -. EMBL; D26508; BAA05514.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                     Fatty aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and/or be involved in metal ion binding.
SIMILARITY: Belongs to the fatty acid desaturase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: The histidine box domains may co and/or be involved in metal ion binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Abundant detectable in root tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phospholipids.

PATHWAY: Polyunsaturated fatty acid biosynthesis.
SUBCELLULAR LOCATION: Endoplasmic reticulum.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its European institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                   118
                                                                                                                                                                              135;
                                                   65
                                                                                58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comment=A number
                                                                                                                                             N
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                                                                                                                                                                                             Similarity
GFVLHSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVFTL
                                                                                                                                                                                                                                                                                                                                                                       ď
                                                 AVAALAIAAVYVD-----SWELWPLYWAAQGTLFWAIFVLGHDCGHGSESDIPLLNSVV
                                                                      AYVFYYLANTYIPLIPTPLAYLAWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIV
                                                                                                                                            GAGGRMS----DPSEGKNILERVPVDPPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIV
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220
242
101
137
137
304
                                                                                                                                                                                                                                                                                                                                                                     biosynthesis;
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                        Alternative
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262
105
141
308
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                                                                                                                                                                                                                                           44076 MW;
                                                                                                                                                                                             30.3%;
34.6%;
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Y: Abundant in leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of isoforms are
                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Endoplasmic reticulum;
                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                    splicing.
POTENTIAL.
                                                                                                                                                                                                                                                       POTENTIAL.
HISTIDINE E
HISTIDINE E
HISTIDINE E
                                                                                                                                                                             Score 620.5; DB 1
Pred. No. 1.1e-42;
7; Mismatches 131
                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                              ---AQPPFKIGDIRAAIPKHCWVKSPLRSMSYVVRD-II
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ISTIDINE BOX-3.
6A7EA2A692B85164
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                                                                                                                                                                                                          Length
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RESULT
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P486Z6;
01-FEB-1996
                                                                                  TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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  DOMAIN
DOMAIN
                                                                                                                                                                    InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster
lamiids; Solanales; Solanaceae; Nicotiana.
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01-FBB-1996 (Rel. 33, Last sen
28-FBB-2003 (Rel. 41, Last ann
Omega-3 fatty acid desaturase,
                                                                                                                                                                                                                                 EMBL; D26509; BAA05515.1; PIR; JC2555; JC2555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
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MEDLINE=95011632;
                                                                TRANSMEM
                                                                                                                             Transmembrane
                                                                                                                                              Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of a cDNA encoding tobacco
Gene 147:293-294(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   phospholipids.

PATHMAY: Polyunsaturated fatty acid biosynthesis.

SUBCELLULAR LOCATION: Endoplasmic reticulum.

DOMAIN: The histidine box domains may contain the active and/or be involved in metal ion binding.

SIMILARITY: Belongs to the fatty acid desaturase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: ER (microsomal) omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 18:3 fatty acids, important constituents of plant membranes. It is thought to use cytochrome b5 as an electron donor and to act on fatty acids esterified to phosphatidylcholine and, possibly, other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345
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                                                                                                                                                                PD001081;
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Kodama H., Nishimura M
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biosynthesis;
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BOX-1.
BOX-2.
BOX-3.
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Ak Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,
Ak Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
Reldmann K.A., Pierce J., Browse J.;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
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                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
ty acid desaturase, chloroplast precursor
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Pred. No. 5.4e-42;
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Best Local :
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NON TER
TRANSIT
CHAIN
DOMAIN
                                     STRAIN=cv. Columbia; TISSUE=Hypocotyl;
MEDLINE=94302147; PubMed=8029334;
Yadav N.S., Wierzbicki A., Aggerter M., Caster C.S., Perez-Grau
Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L
Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H
Feldmann K.A., Pierce J., Browse J.;
"Cloning of higher plant omega-3 fatty acid desaturases.";
Plant Physiol. 103:467-476(1993).
                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cmega-3 fatty acid desaturase, chloroplast precursor FAD7 OR FADD OR AT3G11170 OR F9F8 4 OR F11B9.10.
                                                                                                                                                                                                                                                                                                                  FD3C ARATH
                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
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DOMAIN
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Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
Oxidoreductase; Fatty_acid_biosynthesis;
SEQUENCE FROM N.A. STRAIN=cv. Columbia;
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PIR; PQ0812; PQ0812.
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199
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RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Wincker P., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Sundonati B.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Sindonati B.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Sindonati B.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Sindonati B.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Sindonati B.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
ROOKER, J. Ludde M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Navarro P., Collado C., Perez-Perez A., Cottet A., Casacuberta E.,
RA Monifort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Monifort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Monifort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Taulon L.J., Jenkins J.,
RA Mannhaupt G., Haase D., Schoof H., Tullon L.J., Jenkins J.,
RA ROONey T., Riazo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Riazo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Riazo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Raas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Paies C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto M., Matsunio A., Muraki A.,
RA Watanabe A., Yamada M., Ya
                                                                                                             EMBL; L22961; AAA61773.1; --
EMBL; D14007; BAA03106.1; --
EMBL; D26019; BAA05040.1; --
EMBL; AC009991; AAF01508.1;
EMBL; AC073395; AAG50977.1;
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Iba K., Gibson S., Nishiuchi T., Fuse
Hugly S., Somerville C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol PATHMAY: Polyunsaturated fatty acid biosynthesis. SUBCELLIULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). SUBCELLIULAR SPECIFICITY: Most abundant in leaves and seedlings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: The histidine box domains may contain the active and/or be involved in metal ion binding. SIMILARITY: Belongs to the fatty acid desaturase family.
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an email to license@isb-sib.ch).
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v. Columbia; TISSUE=Hypocotyl;
M., Yamamoto K.;
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0487; FA_desaturase;
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MEDIJNE-94302147; PubMed-8029334;

Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,

Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,

Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,

Feldmann K.A., Pierce J., Browse J.;

"Cloning of higher plant omega-3 fatty acid desaturases.";

Plant Physiol. 103:467-476(1993)

-I- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the

third double bond in the biosynthesis of 16:3 and 18:3 fatty

acids, important constituents of plant membranes. It is thought to

use ferredoxin as an electron donor and to act on fatty acids

esterified to galactolipids, sulfolipids and phosphatidylglycerol.

-i- PANTHWAY: Polyunsaturated fatty acid biosynthesis.
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Spermatophyta; Magnoliophyta;
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Matches 128
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P48622;
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01-FEB-1996 (Rel. 33, Last seq
28-FEB-2003 (Rel. 41, Last ann
Temperature-sensitive omega-3
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PIR; JQ2339; JQ2339.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
Oxidoreductase; Fatty acid_biosynthesis; Chloroplast; Membrane;
                                                                                                             precursor (EC 1.14.19.-).
FAD8 OR AT5G05580 OR MOP10.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                ARATH
 SEQUENCE FROM N.A
                         NCBI_TaxID=3702;
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SIMILARITY: Belongs to the fatty acid desaturase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). DOMAIN: The histidine box domains may contain the active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its European Bioinformatics Institute. There are no restrictions on its European Bioinformatics Institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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Pred. No. 3.9
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HISTIDINE BOX-2.
HISTIDINE BOX-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibson S., Arondel V., Iba K., Somerville C.R., "Cloning of a temperature-regulated gene encoding omega-3 desaturase from Arabidopsis thaliana.", Plant Physiol. 106:1615-1621(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L27158; AAA65621.1; -.
EMBL; U08216; AAB60302.1; -.
EMBL; D17578; BAA04504.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia; TISSUE=Hypocotyl; Watahiki M.C., Yamamoto K.T.; Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desat_fam; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
MEDLINE=97471969; PubMed=9330910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia; TISSUE=Aerial parts; MEDLINE=95148742; PubMed=7846164;
                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                               TRANSIT
                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron domor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol. PATHMAY: Polyunsaturated fatty acid biosynthesis. SUBCCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). INDUCTION: BY LOW TEMPERATURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: The histidine box domains may contain the active and/or be involved in metal ion binding.
SIMILARITY: Belongs to the fatty acid desaturase family.
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196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                          Similarity
                                                       HANTNSLDNDEVYIPKRKSKVKIYSKLLNNPPGRVPTLVFRLTLGFPLYLLTNISGKKYG
                                                                          AWPVYWFCQASILTGLWVIGHECGHHAFSDYQLIDDIVGFVLHSALLTPYFSWKYSHRNH
                                                                                                                  PPENLADIRAAIPKHCWVKNPWMSMSYVVRDVAIVEGLAAVAAYENN----
                                                                                                                                 PPFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAY----VFYYLANTYIPLIPTPLAYL
HONHGHVENDESWHPLPES---IYKNLEKTTOMFRFTLPFPM-LAYPFYLWNRSPGKQ--
                                                                                                                                                                                                                                    156
192
359
435
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196 HI
363 HI
50136 MW;
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DESATURASE.
HISTIDINE BOX-1.
HISTIDINE BOX-2.
HISTIDINE BOX-3.
HISTIDINE BOX-3.
                                                                                                                                                                           Score 598.5; DB 1
Pred. No. 7.8e-41;
7; Mismatches 127
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Search Job ti	DЬ	ğ	DЬ	Ş	DЬ	Ş	Дb	Ş
Search completed: June 18, 2004, 17:36:55 Job time : 20 secs	427 D 427	363 p 363	367 QIPHYHLVEATEAAKPVLGKYYREPKNSGPLPLHLLGSLIKSMKQDHFVSDTGDVVYYEA 426		308 WIDFVTYLHHHGHEDKLPWYRGKEWSYLRGGLTTLDRDYGWINNIHHDI-GTHVIHHLFP 366	260 FFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLNRVFHDVTHTHVLHHLIS 317	250GSHYHPDSDLFLPKEKKDVLTSTACWTAMAALLVCLNFVMGPIQMLKLYGIPYWIFVM 307	200 REANHFDEMSPIFNDRERVQVLLSDEGLLAVEYAIKLLVAAKGAAWVINMYAIEVLGVSV 259

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Result
No.
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-MODEL-frame+_p2n.model -DEV=xlh
-Q=/Cgn2_1/USPTO_spool/US10069772/runat_18062004_145511_5274/app_query.fasta_1.519
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTEMT=ptc -NORM-exct -HARSIZE=500 -MINLEND=0 -MAXLEND=200000000
-USER=US10069772_@CGN_1 1_352_@runat_18062004_145511_5274 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - nucleic search, using frame_plus_p2n model
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       0 4 D D L B
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   1636
1592.5
1589.5
1578.5
1337.5
1332.5
1332.5
                                                                                                                                                                Score
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ALIGNMENTS

RESULT 1 AAF88311 Feussner I, 01-SEP-1999; 01-SEP-1999; 08-MAR-2001. DE19941609-A1. Calendula officinalis. triglyceride; transgenic plant; Calendula; 22-AUG-2001 AAF88311; AAF88311 standard; DNA; 1285 (IPBP-) IPB INST PFLANZENBIOCHEMIE. officinalis calendulic acid desaturase encoding DNA. calendulic acid desaturase; unsaturated fatty acid; oil; Hornung (first entry) 99DE-01041609 99DE-01041609 Location/Qualifiers /product= "calendulic acid desaturase" 'n Fritsche K, ₽. ds. Peitzsch N, Renz A

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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                       This DNA encodes the Crepis alpina delta 12 acetylenase. This is used in the production of acetylenic compounds. The process comprises treating C18 fatty acids having a double bond at position delta 12 with an acetylenase to form 12-ynoic acids. The acetylenic compounds can be produced by organisms such as oilseed plants, yeast and fungi which are transformed with this acetylenase DNA. These organisms can accumulate these acetylenic compounds which are chemical feedstocks, particularly for coatings, plasticisers and lubricants. The process enables the production of these acetylenic compounds from a renewable resource with high purity and at reasonable cost. (Updated on 25-MAR-2003 to correct field.)
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Sjoedahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New acetylase used for production of crepenynic acid from linoleic acid - derived from Crepis alpina; used for production of acetylenic fatty acids suited for the production of coatings, plastics and lubricants.
                                                                                                                                                                                                                                                                                                                                     Sequence 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 21; 33pp; English.
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P-PSDB; AAW36793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyrTyrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGTGCTCCATGATGTTACACACACTCACGTTATGCATCATCTGTTTTCATACATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgValPheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyrIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATGGAACTGGCTCAGAGGGGCTTTGTCAACAATCGATAGGGACTTTGGGTTCCTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSerHisArgAsnHisHis 140
                                                                                                                                                                                                                                                                                                                                                                                                              GAGCCTGAAAAAGGTAGGGAGTCCAAGGGTGTATATTGGTACAATAAA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCGATAGGACTCCAATTCTGAAAGCAATGTGGAGAGAGGCCAAGGAATGCATCTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGluCysIleTyrIle 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCGATATCACCTACTTGCACCACACCCATCTGTCGTTGCCTCATTATGATTCATCT
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                                                                                                                                                                                                    delta-12-epoxygenase cDNA clone CrepX
                                                                                                                                                                                                                                                                                                                           CDNA; 1312
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Location/Qualifiers 26. .1150

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA clone, designated CrepX, codes for a novel epoxygenase (see AAW79743) of a Crepis sp. (not Crepis palaestina) that has a high CC vernolic acid content. The CrepX gene shows a high degree of homology to the novel Cpal1 delta-12-epoxygenase gene (see AAV3101) of C.

CC palaestina. CrepX cDNA was isolated from a Crepis sp. cDNA library using C crepis alpina acetylenase partial gene sequence (see AAV63101) as grobe. The invention relates generally to novel genetic sequences (see CC AAV63101-03) encoding fatty acid epoxygenases (see AAW79742-44), especially delta-12-epoxygenases or mixed function monooxygenases. These CC especially delta-12-epoxygenases or mixed function monooxygenases. These CC especially oilseed plants such as flax), in particular to convert unsaturated fatty acids to epoxygenated fatty acids. The invention extends to genetically modified oil-accumulating organisms and to the coils derived from them. These oils can be used in production of coatings, cresins, glues, plastics, surfactants or lubricants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1997;
15-APR-1997;
16-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated fatty acid epoxygenase gene - used particularly for transforming plants for producing modified oils for use in, e.g. coatings, resins, glues, plastics, surfactants or lubricants.
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P-PSDB; AAW79743.
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                                                                ValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeu 79
                                                                                                                                                                                                                                            MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal
AlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly
                                           ATCTTCTACTTCCTTGCCAACACATATATCCCTAATCTCCTCTATCCTCTAGCCTACTTA
                                                                                                                     PheGluArgSerVallieArgSerSerTyrTyrValValHisAspLeuIleValAlaTyr 59
                                                                                                                                                               ATGGGTGCCGGCCGT-----GGTCGGACATCGGAAAAGTCGGTCATGGAACGTGTC
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RESULT 4
AAV63101
ID AAV6
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DE Crep
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KW Fatt
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OS Crep
                                 Fatty acid epoxygenase; Cpal2 gene; mixed function monooxygenase; delta-12-epoxygenase; epoxygenated fatty acid; transgenic plant; vegetable oil; oilseed; ss.
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                                                                                                                                                                                                                                                                                   CC This full-length cDNA clone, designated Cpa12, codes for a novel mixed CC function monoxygenase (see AAW79742) of Crepis palaestina that is CC characterised as having delta-12-epoxygenase activity. It was isolated CC from a C. palaestina cDNA library using a Crepis alpina acetylenase CC partial gene sequence (see AAV63104) as probe. The encoded protein CC contains His-rich motifs (see AAW79752-54) that are characteristic of CC mixed function monoxygenases. The Cpa12 gene was shown to be highly CC expressed in developing seeds, with no expression detectable in leaves. CC The invention relates generally to novel genetic sequences (see AAV63101-CC 03) encoding fatty acid epoxygenases (see AAW79742-44), especially delta-CC 12-epoxygenases or mixed function monooxygenases. These provide the means by which fatty acid metabolism can be manipulated in e.g. yeast, mould, CC bacteria, insects, birds, mammals and plants (especially oilseed plants CC such as flax), in particular to convert unsaturated fatty acids to CC epoxygenated fatty acids. The invention extends to genetically modified CC oil-accumulating organisms and to the oils derived from them. These oils can be used in production of coatings, resins, glues, plastics, cx surfactants or lubricants
                                                                                                                                                  US-10-069-772-2 (1-377) x AAV63101
                                                                                                                                                                                                                       Score:
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15-APR-1997;
16-APR-1997;
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(STYM/)
                                                                                                                                                                                                                                                                   Sequence 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 78-81; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated fatty acid epoxygenase gene - used particularly for transforming plants for producing modified oils for use in, e.g. coatings, resins, glues, plastics, surfactants or lubricants.
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STYMNE S.
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                                                       ProValAspPro---ProPheThrLeuSerAspLeuLysLysAlaIleProThrHisCys
           TTCCAGAGATCTGTAATCCGCTCATCTTACTATGTTCAAGATCTCAATTATTGCCTAC
                                                                                                                MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal
                           PheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAlaTyr 59
                                                                                                     ATGGGTGCCGGCGGTCGT-----GGTCGGACATCGGAAAAATCGGTCATGGAACGTGTC
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                                                                                                                                             LysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGluCysIleTyr
                                                                                                                                                                                          CCACACTATCATGCAAAGGAGGCAAGGGATGCAATCAAGCCAATCTTGGGCGACTTTTAT
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(revised) (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes Vernonia galamenensis fatty acid epoxidising enzyme. The present invention also describes: (i) Vernonia galamenensis fatty acid desaturase; (ii) chimeric genes comprising the fragments linked to regulatory sequences; and (iii) transformed host cells containing the chimeric genes. The DNA's from the present invention can be used to alter levels of expression of the enzymes in transformed host cells or to produce the recombinant enzymes by transformation of microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
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No.:
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1364 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding Vernonia galamenensis fatty acid desaturase and fatty acid epoxidising enzyme - used to alter levels of expression of the enzymes in transformed host cells or to produce recombinant enzymes.
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P-PSDB; AAW83354.
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             GGTTTATGGGTCATTGGCCATGAATGTGGCCATCATGCTTATAGTGAGTACCAGTGGGTT
                        GlyLeuTrpVallleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIle
                                                                               ThrProLeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThr
                                                                                                                      GATCTCATTATTACCTTCCTTTATACACGCTCGCCAACTCTTACATTCCTCTTCTTCCT
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                                                   desaturase; transgenic; plant; oil; triglyceride; unsaturated fatty food; animal feed; cosmetic; pharmaceutical; pomegranate; ds; gene; delta-12-desaturase; PuFADI2.
                          Punica granatum
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                                                                                                        granatum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisVal 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerLeuProHisTyrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThr
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel nucleic acid encoding a polypeptide with desaturase activity. The products of the invention are used in the construction of constructs, vectors, organisms and transgenic plants containing the desaturase. The invention also describes methods for preparing oils or triglycerides with increased content of unsaturated fatty acids; oils fats and fatty acid mixtures and a novel nucleic acid encoding a protein able to convert a fatty acid to a more highly unsaturated acid. The products of the invention are used to produce transgenic plants (or other organisms) that produce oils and fats with increased contents of unsaturated fatty acids, useful in preparation of foods, animal feeds, cosmetics and pharmaceuticals and in homology screening for isolation of genomic sequences. This sequence encodes a fragment of the Punica granatum (pomegranate) delta-12-desaturase PuFADI2 described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1398 BP; 311 A; 422 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           risolated nucleic acid encoding desaturase enzymes from pomegranate, ful for recombinant production of unsaturated fatty acids, for e.g. production of food, animal feeds and pharmaceuticals.
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                                                     IleProThrProLeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIle 91
                                                                                          CTCTATGACCTCACTTTGGTGGCCATCTTCTATTACGTTGCTACCACTTACATCGACGCC
                                                                                                                ValHisAspLeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeu
                                                                                                                                                                   LysLysAlaIleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrVal 51
                                                                                                                                                                                                                  AGCCAGAAGCCGGTCCAAAGGGTTCCCTCCGCAAAGCCACCATTCACACTAAGCGAGATC
                                                                                                                                                                                                                                  GlyLysAsnIleLeuGluArgValPro---ValAspProProPhcThrLeuSerAspLeu ::: :::::||||||||||||
                                                                                                                                                                                                                                                                              ATGGGAGCCGGTGGAAGAATGACGGTCCCGAACAAGTGGGAAGGCGAGGGAGACGAGAAG
LeuThrGlyLeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGln 111
                              CTCCCGGGTCCACTACGCTACGCGGCCTGGCCCGTGTACTGGGCCCTGCAGGGGTGCGTG
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Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic linoleic acid; stearic acid; oleic acid; transgenic plant; cotton seed oil; oleoyl-PC delta12-desaturase; FAD2-2; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for modifying the endogenous oil of a cotton plant, to produce cotton seed oil. The method comprises producing a transgenic cotton plant having a gene construct which includes a fatty acid biosynthesis gene operably linked to a promoter sequence capable of conferring expression of the delta9-desaturase (delta9 stearoyl-ACP desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-desaturase) gene in the seed of a cotton plant. The invention is useful for producing cottonseed oil with reduced palmitic and/or lincleic acid content, and increased stearic and/or oleic acid content. The present sequence is cotton oleyyl-PC delta12-desaturase (ghFAD2-2) protein cDNA sequence is cotton oleyyl-PC delta12-desaturase (ghFAD2-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying endogenous oil of cotton plants, to produce cotton seed oil with reduced palmitic and/or linoleic acid content, involves producing transgenic plants containing a fatty acid biosynthesis gene in a
                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1422 BP;
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                                                     ATATTGGCCTCTTTTTTACCATGTGGCCACCAATTACTTCCCTAACCTTCCTCAGGCT
                                                                             IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro
                                                                                                          CCACCACACTGTTTCCAGCGCTCCGTTTTACGCTCATTCTCATATCTCCTTTACGACTTT
                                                                                                                             ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel polypeptide, CoFac2, capable of catalysing the formation of two conjugated double bonds. The products of the invention can be used for the large scale production of conjugated linoleic acids. The composition may be used for cosmectic or pharmaceutical purposes. The conjugated linoleic acids may be used for coating, painting or cold weather ester-type lubricant purposes. There not a natural source which is rich in conjugated linoleic acids and chemical processes result in a mixture of several isomers. Plant biotechnology is cost-effective and renewable with little side effects. This sequence encodes the Calendula officinalis CoFad2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids which encode a conjugase and its related enzyme a de desaturase to be used for the large scale production of conjugated linoleic acid and linolenic acid in plants.
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                                                                                                                                                                                                                                                                                    standard;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to Brassica plants containing recombinant nucleic acid constructs comprising (a) a wild-type microsmal Delta-12 fatty acid desaturase (Fad2) coding sequence linked to a regulatory sequence and (b a wild-type microsmal Delta-15 fatty acid desaturase (Fad3) coding sequence linked to a regulatory sequence. The plants exhibit a seed-specific reduction in native Fad2 and Fad3 gene expression. The plant produces seeds yielding an oil whose fatty acids comprise at least 86 percent oleic acid and less than 2 percent erucic acid. The plants are used to produce cannola (rapeseed) oil having a high oleic acid content, low erucic acid content, a low alpha-linolenic acid content and high oxidative stability. The present sequence represents the coding sequence of the F form of the wild-type Fad2 gene
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity:
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                                            CTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAAGGGTGCGTCCTAACCGGCGTC
                                                                                                                                           LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysLysAlaIle
                 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer
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| GGCTACCGTTGACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to fatty acid desaturases (FAD) from Brassicaceae or Helianthus, where the FAD genes comprise at least one mutation in their sequences. The mutation is in a region encoding the His-Xaa-Xaa-Xaa-His motif of the delta-12 or delta-15 fatty acid desaturases. The invention also provides methods for producing the FAD mutant genes and gene products. The products can be used for producing plants and seeds which have altered fatty acid compositions, e.g. an elevated oleic acid content, a decreased, stabilised linoleic acid content, both elevated oleic acid and decreased, stabilised linoleic acid content or a decreased, stabilised linoleic acid and increased level of linoleic acid and increased level of linoleic acid. The plants may be e.g. soybean, rapeseed, sunflower, safflower, castor bean or corn. The present sequence represents the DNA sequence of the coding region of the Brassica wild-type Fad2-F gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity:
/ Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1155 BP; 246 A; 361 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated mutant fatty acid desaturase genes - obtained by mutation Brassicaceae or Helianthus plants, used for producing plants or seeds having altered fatty acid compositions.
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                IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer
                                                                              TrpVallleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAsp
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                                                                                                                                                  LeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu
 ACCGTCGGTCTCATCTTCCACTCCTTCCTCCTCGTCCCTTACTTCTCCTGGAAGTACAGT
                                                              TGGGTCATAGCCCACGAGTGCGGCCACCACGCCTTCAGCGACTACCAGTGGCTTGACGAC
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                                                                       Long chain monounsaturated fatty acid; erucic acid; oleic acid; delta-15 fatty acid desaturase; Fad3; linoleic acid; vegetable oil; industrial oil; lubricant; hydraulic oil; delta-12 fatty acid desaturase; Fad2; Fad2-F; rapeseed; ds.
                                                                                                                                       B. napus Delta-12 fatty acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      CC comprising a Bequence encoding a plant enzyme that is a delta-12 (C desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.) CC Chimeric genes comprising nucleic acids of the invention are used to CC create transgenic plants with altered levels of unsaturated fatty acids, and can modify plant lipid composition. Nucleic acids of the invention CC can be used as hybridisation probes to isolate or amplify nucleotide cc sequences encoding other fatty acid desaturases or fatty acid desaturase. CC related enzymes. They can also be used in restriction fragment length CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in CC seed oil of oil producing plant species. They can also be used to produce seed oil containing altered levels of unsaturated fatty acids. Nucleic cacids of the invention can combine the high oleate trait of transformed CC seed with mutations for altered fatty acid compositions to obtain new CC total saturates and high in monounsaturates would provide significant CC health benefits to consumers (reduced risk of Coronary heart disease) as well as economic benefits to oil processors. The current sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, delta-12 fatty acid hydroxylase for creating transgenic plants and producing seed oil with altered levels of unsaturated fatty acids.
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15-OCT-1993;
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                                                                                                                      ATC---AAGCGCGTACCCTGCGAGACACCGCCCTTCACTGTCGGAGAACTCAAGAAAGCA
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                                                                                                                                                                                                                                                       Sequence 1464
                                                                                                                                                                                                                                                                                                 diagnostic markers in plant genetic mapping and plant breeding programs. In addition (I) may be used to isolate other related FAD genes. The present sequence represents a Brassica napus CDNA which encodes the wild
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                                                                   CC in plant seeds and comprising a seed-specific regulatory sequence linked to ceither a mutant delta-12 or delta-15 fatty scid desaturase (FAD) gene CC either a mutant delta-12 or delta-15 fatty scid desaturase (FAD) gene CC encoding a protein with a mutation in a His-(ABD)dil)-Cys-(GlyAhla)-His CC amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15 CC FAD. Expression of this construct in plants decreases the level of CC activity of these enzymes in the cells of the plant i.e. the construct CC gene is used to decrease the level of linoleic acid in the seeds of CC glants to (soybean, rapeseed, sunflower, oil palm, coconut palm, flax, CC setor and peanut) Similarly a construct comprising a mutant delta-15 CC gene is used to decrease the levels of lapha-linolenic acid in the seeds of CC gene is used to decrease the levels of palm, coconut palm, flax, CC gene is used to decrease the levels of alpha-linolenic acid in the seeds of CC plants, especially Brassica canola. The new method may also be used to the levels of both linoleic and alpha-linolenic acid simultaneously in CC their seeds. These methods alter the nutritional value of the seeds of CC diagnostic markers in plant genetic mapping and plant breeding programs. CC diagnostic markers in plant genetic mapping and plant breeding programs. CC mutant D form of microsomal delta-13 farty acid desaturates of CRNAP) comprises the sequence represents a Brassica napus CNNA which encodes the mutant D form of microsomal delta-13 farty acid desaturates of CRNAP)
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Sequence 1155 BP;
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ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHis
                                                                                                               ValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSer
                                                                                                                                                                                                           GACCGCGAGCGTCTCCAGATATACATCTCCGACGCTGGCATCCTCGCCGTCTGCTACGGT
                                                                                                                                                                                                                      AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla
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                                                       LeuProHisTyrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp
                                                                                               CTCTACCGCTACGCTGCTGCCAAGGAGTTGCCTCGATGGTCTGCTTCTACGGAGTTCCG
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CC This DNA sequence codes for canola microsomal delta-12 fatty acid CC desaturase (PAD) F form (see AAW24997). Plants are claimed that contain a CC mutation in the delta-12 FAD gene. A preferred mutation is in the region CC encoding a conserved motif (see AAW24994) of delta-12 FADs. A T to A CC transversion at nucleotide 515 of the canola delta-12 FAD gene (see CC AAT85849) results in a Leu to His amino acid substitution that CC contain the enzyme and alters the fatty acid composition of the seed CC oil (see AAW24998). Mutant plants, preferably canola and sunflower, that CC contain the mutation are obtained by conventional mutagenesis of plant CC canother conserved motif (see AAW24996) of delta-12 FAD and also into CC delta-15 FAD. The mutant plants produce oils of low saturated fatty acid content (maximum 5%, with not over 2% erucic acid), high oleic acid content (at least 71%) and low linoleic acid content. The content of CC palmitic acid may be high or low. The vegetable oils can be used in food production and should help to reduce the incidence of coronary heart CC field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 12; Page 71-72; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutated Brassica or Helianthus delta-12 or -15 fatty acid desaturase genes - and plants containing them, having altered fatty acid content seed oil, especially low saturates but high oleic acid content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1995;
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          ValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSer
                                                                                                                                               GACCGCGAGCGTCTCCAGATATACATCTCCGACGCTCGCCATCCTCGCCGTCTGCCTACGGT
                                                                                                                                                              AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla
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CTGCCTCACTATGACTCGTCTGAGTGGGATTGGTTGAGGGGAGCTTTGGCCACCGTTGAC
                                                                                                                       IleLysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIlePro
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                                                CTCTACCGCTACGCTGCTGTCCAAGGAGTTGCCTCGATGGTCTGCTTCTACGGAGTTCCG
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Search completed: June 23, 2004, 15:58:02 Job time: 389 secs

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Result
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-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG SCORES=0 -MATT -DSEBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6
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US-09-354-2318-13
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APPLICANT: SJODAL, Staffan
APPLICANT: STYME, Sten
APPLICANT: LENMAN, Marit
TITLE OF INVENTION: NOVEL PLANT ENZYME AND
FILE REFERENCE: BAFOR=1
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BANAS, Antoni
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US-09-059-769-3
                                                                                                                    US-09-059-769-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 base pairs
LENGTH: nucleic acid
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APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/
PILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
PILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
APPLE ENTRY DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/059,7
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6226
APPLICATION NUMBER: AU PO6226
                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Crep
FEATURE:
NAME/KEY: CDS
LOCATION: 26...
                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    MOLECULE TYPE:
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STATE: Colora
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ferber, Donna M. REGISTRATION NUMBER:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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ID NO: 3:
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US-10-069-772-2 (1-377)
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LysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGluCysIleTyr 359
                                                               ProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyrTyr 339
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                                                                                                                                         AsnArgValPheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyrIle
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                                                                                                                 AATAGTGTTTTCCATGATGTNACACACACTCACGTCATGCATCATTTGTTTTCATACATT
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APPLICANT: Singh, Surinder
APPLICANT: Stenman, Marit
APPLICANT: Stenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Plant Fatty Acid Ep
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                  TELEPAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
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                                                                                                                                                                       FEATURE:
                                                                                                                                                                                      MOLECULE TYPE:
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APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
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FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and
STREET: 5370 Manhattan Circle, 6
                                                                                                                                          NAME/KEY:
LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-872-302-3
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
FEATURE:
NAME/KEY: CD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Majarian, William R
REGISTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-1084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEPAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Fatty Acid TITLE OF INVENTION: Developing NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1007 Mark
CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/872,302
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ThrProLeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThr
                                                                       AspLeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIlePro
                                                                                                                          AlaIleProThrHisCysPheGluArgSerVallleArgSerSerTyrTyrValValHis
                                             GATCTCATTATTACCTTCCTTTATACACGCTCGCCAACTCTTACATTCCTCCTTCTTCCT
                                                                                                         GCAATCCCTCCGCATTGCTTCCAGCGATCTGCCATCCGTTCATCGTGCTACGTTGTTCAG
                                                                                                                                                                 AATATAAACGAACGTGCACCGGTTGATGCGGCACCATTCTCGTTAAGCGATCTAAAGAAA
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Seeds of Vernonia
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Matches:
Conservative:
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Indels:
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Sequence 1, Application US/08675650B Patent No. 5850026
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CANOLA OIL HAVING INCREASED OLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Brassica napus FEATURE: OTHER INFORMATION: Wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,650B
FILING DATE: 03-JUL-1996
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HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 37,875
REFERENCE/DOCKET NUMBER: 07148/042001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 60 South & CITY: Minneapolis
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ACCGTCGGTCTCATCTTCCÁCTCCTTCCTCCTCGTCCCTTÁCTTCTCCTGGAAGTACAGT
                     IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer
                                                                       TGGGTCATAGCCCCACGAATGCGGCCACCACGCCTTCAGCGACTACCAGTGGCTTGACGAC
                                                                                                                                                                                                                              CACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCTCCTACCTCATCTGGGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLys-----AsnIle
                                                                                               TrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAsp
                                                                                                                                                                                      LeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu
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Indels:
Gaps:
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Matches:
Conservative:
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RESULT 5 US-08-675-650B-1

GENERAL INFORMATION:
APPLICANT: DeBonte, I
TITLE OF INVENTION: OF INVENTION: OF INVENTION: OF SEQUENCES:
CORRESPONDENCE ADDRESS

ADDRESSEE:

ADDRESS:

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GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: FATTY ACID DESATURASES AN
FILE REFERENCE: 07148-063002
CURRENT APPLICATION NUMBER: US/09/354,231B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR PILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-354-231B-13
                                     SEQ ID NO 13
LENGTH: 1155
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TYPE: DNA
ORGANISM: Brassica
FEATURE:
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APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072001
CURRENT APPLICATION NUMBER: US/09/128,602B
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version 4.0
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TYPE: DNA
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Sequence 13, Application US/09995297
PATENT NO. 6649782
GENERAL INFORMATION:
APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
TITLE OF INVENTION: PATTY ACID CONTENT
FILE REFERENCE: 07148-072002
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Best Local Similarity:
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CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR FILING DATE: 1998-08-03
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SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Brassica
FEATURE:
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           ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle
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GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: FATTY ACID DESATURASES AN
FILE REFERENCE: 07148-063002
CURRENT APPLICATION NUMBER: US/09/354,231B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US/08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
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Best Local Similarity:
                                                                                                                                                                                                   Pred. No.:
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                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1)
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                                                                                                                                                                                                                                                                                                          TYPE: DNA
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ValLeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGlu
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US-09-128-602B-9
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GENERAL INFORMATION:
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APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: FLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072001
CURRENT APPLICATION NUMBER: US/09/128,602B
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...
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GTGATGTTAACGGTTCAGTTCACTCTCGGCTGGCCTTTGTACTTAGCCTTCAACGTCTCG 597
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                                                        LysArgLysSerLysValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgVal 174
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                                                                                                                                                                                              AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyr 134
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                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: Pan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072002
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                                                                                                    TYPE: DNA
ORGANISM: Brassica r
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(119
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                                                                           ValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSer
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ValLeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGlu
                                         HisLeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysPro
                                                                                                                                                 LeuProHisTyrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp
                                                                                                                                                                                IleLysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIlePro
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:: 234 Int Similarity: 76.44\$ Conservative: 58 Local Similarity: 61.26\$ Mismatches: 82 F. Match: 64.34\$ Indels: 8 Gaps: 4	LD NO: 3:	WISM: Brassica napus 3/KEY: CDS WION: 1301284	linear cDNA to m	H 4. 6 4	TELEPHONE: (302)992-5481 ; TELEFAX: (302)773-0164 ; TELEX: 835420 ; INFORMATION FOR SEO ID NO: 3:	NAME: CHRISTENBURY, LYNNE M. REGISTRATION NUMBER: 30,971 REFERENCE,DOCKET NUMBER: BB-1043-D TELECOMMUNICATION INFORMATION.	PRIOR APPLICATION DATA: APPLICATION NUMBER: U.S. 07/977,339 FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION:	9/133,96	MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE COPERATING SYSTEM: MICROSOFT WORD FOR MINDOWS 95 SOFTWARE: MICROSOFT WORD VERSION 7.0A	STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA ZIP: 19898 COMPUTER READALE FORM:	CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: B. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON	o 2	H 2. 0	RESULT 12 US-09-133-962A-3 ; Sequence 3, Application US/09133962A	Oy 374 TyrHis 375	Qy 354 AlalysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTrp 373	Db 1018 ATACTGGGAGAGTATTATCAGTTCGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAG
	294 1027			Qy 234 IleLysLeuLeuValAlaAlaLys	Qy 214 AspArgGluArgValGlnValLeu	Qy 195 GlyLysLysTyrGlyArgPhe	Qy 175 PheThrLeuValPheArgLeuThr	Qy 155 LysargLysSerLysValLysIle	Qy 135 SerHisArgAsnHisHisAlaAsn 1	Qy 115 AspIleValGlyPheValLeuHis	Qy 95 LeuTrpValIleGlyHisGluCys	Qy 75 ProLeuAlaTyrLeuAlaTrpPro	Qy 55 LeuIleValAlaTyrValPheTyr	Qy 35 IleProThrHisCysPheGluArg		. 13 : -	-10-069-77
	ArgAmpheGlyPhoLeuAsmArgValPheH.sAsgValThrHisThrHisValLeuHis 313 ::: :::: ::::			IleLysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIlePro 253 :::	AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233	GlyLysLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213	PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSer 194	LysArgLysSerLysValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgVal 174 :::	SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIlePro 154	AsplevalGlyPhevalLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyr 134	LeuTrovalIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAsp 114 :::	ProLeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGly 94 ::: :::	LeuileValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuileProThr 74 ::: ::: ATCATCATAGCCTCCTGCTTCTACTACGCCCACCACCTTACTTCCCTCCTCCCTC	TleProThrHisCysPheGluArgSerVallleArgSerSerTyrTyrValValHisAsp			

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RESULT 13
US-09-354-231B-11
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Best Local Similarity:
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PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 11
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APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: FATTY ACID DESATURASES
FILE REFERENCE: 07148-063002
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NAME/KEY: CDS
LOCATION: (1).
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TYPE: DNA
ORGANISM: Brassica
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                                                                                                      LeuileValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThr 74
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                                              GACACCGTCGGCCTCATCTTCCACTCCTTCCTCCTCGTCCCTTACTTCTCCTGGAAGTAC
                                                                    AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyr
                                                                                                                                                                  CCTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAGGGCTGCGTAACCGGC
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                    154
 ; NAME/KEY: CDS
; LOCATION: (1)
US-09-128-602B-11
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                                                                                                                                APPLICANT: Kodali, Dharma
APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: Pean, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS H
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072001
CURRENT APPLICATION UNMBER: US/99/128,602B
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
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                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 11
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                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09128602B Patent No. 6414223
                                                         TYPE: DNA
ORGANISM: Brassica
                                                FEATURE:
                                                                                         LENGTH: 1155
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CTGCCTCACTATGACTCGTCTGAGTGGGATTGGTTGAGGGGAGCTTTGGCCACCGTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
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APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
APPLICANT: DeBonte, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
TITLE OF INVENTION: FLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
FILE REFERENCE: 07148-072002
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                           GCGAAGGAGTGTATCTATGTGGAACCGGACAGGCAAGGTGAGAAGAAAGGTGTGTTCTGG
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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
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-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB

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APPLICANT: Lemman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GE:
TITLE OF INVENTION: FATTY ACID METABOLISM
FILE REFERENCE: 26-98A
CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
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APPLICANT: Singh, Surir
APPLICANT: Lenman, Mari
APPLICANT: Stymne, Ster
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 1199
TYPE: DIA
ORGANISM: Vernonia galamensis
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LOCATION: (44)..(11
OTHER INFORMATION:
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                                                                                   TACGAACGTTTTGCCAACCATTTTGATCCCATGAGTCCCATTTTCACCGAGCGTGAGCAT
                                                                                                 TyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArg
                                                                                                                                   GCTTTCAGATTGATCGTGGGTTTTCCTTTATACCTTTTCACCAATGTTTCAGGCAAGAAA
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                                                                                                                                                                                                SerLysValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeu
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Percent Similarity:
Best Local Similarity:
                                                             Alignment Scores: Pred. No.:
                                                                                                                       NAME/KEY: misc feature; LOCATION: (901)..(901); OTHER INFORMATION: N iu US-09-981-124-3
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APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID METABOLISM
FILL REFERENCE: 26-98A
CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-16
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6223
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR PILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR PILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEO IT NOS: 24
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SOFTWARE: PatentIn version
SEQ ID NO 3
LENGTH: 1309
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                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: (937)... (937) other Information: N is a NAME/KEY: CDS LOCATION: (26)... (1147) other INFORMATION:
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Crepis
FEATURE:
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                                                  ASDĀTGValPheHiSASDValThrHiSThrHiSValLeuHiSHiSLeuIleSerTyrIle
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FILE REFERENCE: 26-98A
CURRENT FILING DATE: 2001-10-17
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1998-04-16
PRIOR FILING DATE: 1997-04-16
PRIOR PRILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: AU P06223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU P06226
PRIOR APPLICATION NUMBER: AU F06226
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
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Best Local Similarity:
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US-09-981-124-1
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APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID EPOXYGENASE
TITLE OF INVENTION: FATTY ACID METABOLISM
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NAME/KEY: CDS
LOCATION: (30)..(11
OTHER INFORMATION:
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                                                           ATCTTCTACTTCCTTGCCAACACATATATCCCTACTCTTCCTACTAGTCTAGCCTACTTA
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                  AlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly 99
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RESULT 4
US-10-425-114-14778
Sequence 14778, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Chou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION UNBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28
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; OTHER INFORMATION:
US-10-425-114-14778
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APPLICANT: Cao Yongwei
FITTLE OF INVENTION: Soy Nucleic Acid Molecul
FITTLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21(52223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 285684
SEQ ID NO 123945
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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OTHER INFORMATION: Clone ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
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 LeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu 95
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                                                            LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysLysAlaIle
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APPLICANT: Fillatti, JoAnne
TITLE OF INVENTION: Intron Double Stranded RN
FILE REFERENCE: 16517.266
CURRENT APPLICATION NUMBER: US/10/465,800
CURRENT FILING DATE: 2003-06-20
FRIOR APPLICATION UNMBER: US 60/390,186
PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 55
SOFTMARE: Patentin version 3.1
SEQ ID NO 3
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TYPE: DNA
ORGANISM: Glycine
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CURRENT APPLICATION NUMBER: US/10/176,149
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/151,224
PRIOR FILING DATE: 1999-08-26
PRIOR RELICATION NUMBER: US 60/172,128
PRIOR REFLICATION NUMBER: US 09/638,508
PRIOR APPLICATION NUMBER: US 09/638,508
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-069-772-2 (1-377) x US-10-176-149-3 (1-6220)
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APPLICANT: Fillatti, Joanne, J.
APPLICANT: INVENTION: Nucleic Acid Sequences and Methods of Use for the Production
TITLE OF INVENTION: with Modified Polyunsaturated Fatty Acids
FILE REFERENCE: 16518.056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10176149 Publication No. US20030172399A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5574 CATTACACTTCCTCTGAGTGGGACTGGTTGAGAGGAGCTTTAGCAACAGTGGATAGAGAT
                                    LeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu
                                                                                                                        LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysLysAlaIle
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Sequence 12782, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
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US-10-425-114-12782
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; LENGTH: 1457
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; ORGANISM: Glycine max
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; OTHER INFORMATION: Clone II
US-10-425-114-12782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Liu, Qing
TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
FILE REFERENCE: 45-00
CURRENT APPLICATION NUMBER: US/09/837,751
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,124
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Gossypium
FEATURE:
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LOCATION: (98
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    LeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu
                            ATATTGGCCTCTTTTTTACCATGTGGCCACCAATTACTTCCCTAACCTTCCTCAGGCT
                                      IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro
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                                                                                                                        CTGAAGCGAGTTCCATACTCAAAGCCACCCTTCACTCTGAGTGAAATCAAGAAAGCCATC
                                                                                                                                   LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysLysAlaIle
                                                                                                                                                                      MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLys----
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GENERAL INFORMATION:
APPLICANT: Qiu, Xiao
TITLE OF INVENTION: PRODUCTION OF CONJUGATED LIN
TITLE OF INVENTION: LINOLENIC ACIDS IN PLANTS;
TILE REFERENCE: BNZ-002
CURRENT APPLICATION NUMBER: US/09/852,399
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION UNBER: USSN 60/203,027
PRIOR FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 4
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                                                                                        GlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLys 355
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GAGTGTCTCTACGTTGAACCAGATGAGGGCGACAAGGATAAAGGTGTGTTTTGGTTT 1234
                                    GluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTrpTyr 374
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; LOCATION: (89)...(1237)
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TYPE: DNA
ORGANISM: Calendula (
FEATURE:
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LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeu
                                                                                  CGCGAACGGGCTCAAATCTTCATATCCGACGCCGGGATCTTAGCCGTAGTCTTCGTACTC
                                                                                                            ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle
                                                                                                                                          GGCCGTTACTACGACCGGTTCGCGTGCCATTTCGACCCGAATAGCCCGATCTACTCGAAG
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                           TTCCGACTCGCAATGACCAAAGGGCTCACGTGGGTCCTAACCATGTACGGTGGCCCGTTA
                                                      LysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIleProVal 254
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-09-995-297-13
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Best Local Similarity:
Query Match:
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US-09-995-297-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072002
CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR PRIOR PRIOR DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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| IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro
                                                                 ProThrHisCysPheGluArgSerVallleArgSerSerTyrTyrValValHisAspLeu 55
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                                                                                                                                                                                               MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLys-----AsnIle
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                                                  CCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCTCCTACCTCATCTGGGACATC
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US-09-771-904-13
Sequence 13, Application US/09771904
Publication No. US20030131379A1
GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Fan, Zhegong
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; TITLE OF INVENTION: EATTY ACID DESATURASES AN
; FILE REFERENCE: 07148-063003
; CURRENT APPLICATION NUMBER: US/09/771,904
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Brassica
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LOCATION: (1)...(1152)
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                                  ArgLysSerLysValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPhe
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 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle
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APPLICANT: KOALANT.

APPLICANT: KOALANT.

APPLICANT: FAI, Zhegong

APPLICANT: DeBonte, Lorin R.

TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN TITLE OF INVENTION: PATTY ACID CONTENT

FILE REFERENCE: 07148-072002

CURRENT APPLICATION NUMBER: US/10/715,100

CURRENT FILING DATE: 2003-11-17

PRIOR APPLICATION NUMBER: US/09/995,297

PRIOR APPLICATION NUMBER: US/09/995,297

PRIOR FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: US 09/128,602

PRIOR FILING DATE: 1998-08-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FRENSEQ for Windows Version 4.0
                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN
TITLE OF INVENTION: PARTY ACID CONTENT
FILE REFERENCE: 07148-072002
CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
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APPLICANT: Fan, Z
APPLICANT: DeBont
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                                              GACACCGTCGGCCTCATCTTCCACTCCTTCCTCGTCCCTTACTTCTCCTGGAAGTAC
                                                                    AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyr 134
                                                                                                                                                                                                                                                                                                     IleLeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysLysAla
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                                                                                     APPLICANT: DeBonte, Lorin R.
APPLICANT: Miao, Guo-Hua
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEC
FILE REFERENCE: 07148-663003
CURRENT APPLICATION NUMBER: US/09/771,904
CURRENT FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 9
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Publication No. US20030131379A1
GENERAL INFORMATION:
 NAME/KEY: CDS
LOCATION: (1)...
                                            ORGANISM: Brassica napus
                                                          LENGTH: 1155
TYPE: DNA
                              FEATURE:
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gTCTGGGTCATAGCCCACGAGTGCGGCCACCACGCCTTCAGCGACTACCAGTGGCTGGAC
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                                                              GlyLysLysTyr---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn
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                                 LeuProHisTyrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp
                                                                                                           CTCTACCGCTACGCTGTCCAAGGAGTTGCCTCGATGGTCTGCTTCTACGGAGTTCCT
                                                                                                                                                                  AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla
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ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHis
                   CTGCCTCACTATGACTCGTCTGAGTGGGATTGGTTGAGGGGAGCTTTGGCCACCGTTGAC
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Search completed: June 23, 2004, 18:36:31 Job time: 428 secs

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-Q0-/GGR2 1/USPTO_spool/US1069772/runat_18062004_145512_5295/app_query.fasta_1.519
-Q1-/GGR2 1/USPTO_spool/US1069772/runat_18062004_145512_5295/app_query.fasta_1.519
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-USER=US10069772_GCGN 1 1_2607_grunat_18062004_145512_525 -NCPU=6 -ICPU=6
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-USER=US10069772_WCGN 1 1_2607_WCMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0!5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

REFERENCE	SOURCE ORGANISM	KEYWORDS	ACCESSION	LOCUS DEFINITION	RESULT 1 AY104050
Eukaryota; Viridiplantae; Streptophyta; Embaryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 1856)	Zea mays	HTC.	AY104050	AY104050 1856 bp mRNA linear HTC 16-OCT-2002 Zea mays PCO088038 mRNA sequence.	

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If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.rigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design Overgo Probes
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/mol_type="mRNA"
/db_xref="MaizeDB:634972"
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Genomic Organization of Fatty A
Unpublished (2001)
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 University of Illinois
1102, S. Goodwin Ave., Urbana,
Tel: (217) 333-9643
Fax: (217) 333-9817
                                                               Contact: Dr. Torbert Rocheford Torbert Rocheford
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Seq primer: M13 *~~~
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GlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAlaAlaLysGlyAlaAlaTrp
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QGF7F12, mRNA 8
                                                                                                                                                                                                          http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
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Lactuca sativa
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EST.
                                                                                                                                                                                   Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig2502, see http://cgpdb.ucdavis.
                                                                                                                                                                                                                                                                  Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD)
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                                                              HisAlaLysGluAlaArgAspAlaIle 331
                                                                                                                                  PheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyrIleProHisTyr
                                                                                                                                                                                                                 AsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsnArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TISSUE-germinating seeds
TAG_LIB=QG_EFGHJ_lettuce serriola
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LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysLysAlaIle

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                                                       US-10-069-772-2 (1-377) x CK269848
                                                                                                Query Match:
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Best Local Similarity:
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1 (bases 1 to 99)
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1 (Bases 1 to 99)
2 (Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CK269848 989 bp mRNA linear EST 12-DEC-
EST715926 potato abiotic stress cDNA library Solanum tuberosum
clone POACP38 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: potato-array@tigr.org
Clones can be requested from TIGR via
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum tuberosum
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                  MetGlyAlaGlyGlyArgMetSerAspProSer----
ATGGGAGCTGGTGGTCTATGTCTGCTCCAAATGGCGAGACTGAAGTAAAGAAGAATCCT
                                                                                                                                                                                                           , .989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="abiotic stress treated leaf and root tissue"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (Dases 1 to 973)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue
                                                                                                  Solanum tuberosum (potato)
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Other EST8: EST709015
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: potato-array@tigr.org
Clones can be requested from
TATTGCTACATTGCGTGGCCTATTTACTGGATTTGCCAGGGTTGTGTTTTGCACTGGTATT
                                                                                                   LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysLysAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetGlyAlaGlyGlyArgMetSerAspProSer------GluGlyLysAsnIle 16
                                              LeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu 95
                                                                                                                                                                                                                                         ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu
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primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          four separate sets of plants. Set 1 involved saturation of the soil with 150 mM Nacl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and hear stressed by placement at 3 C. Heat then were heat stressed by placement at 3 C. Heat stressed dat 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed at 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed froots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="abiotic stress treated leaf and root t /lab_host="DH108-TODA" |
/lab_host="DH108-TODA" |
/clone_libe"potato abiotic stress cDNA library" |
/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: |
supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle C for 3-4 weeks. Abiotic stress conditions were appl
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/cultivar="Kennebec"
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               Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                    1 (bases 1 to 725)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                            BQ866257 725 bp
QGC7H15.yg.abl QG ABCDI lettuce
QGC7H15, mRNA sequence.
BQ866257 BQ866257.1 GI:22251722
                                                                                            Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                         http://compgenomics.ucdavis.edu/
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 akozik@atgc.org
   [michelmore@vegmail.ucdavis.edu]
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US-10-069-772-2 (1-377) x BQ866257 (1-725)
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Best Local Similarity:
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                                                                                                                                                                                                                     ValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSerHisArgAsnHis
                                                                                                                              HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLysSerLys 159
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                            ValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPhe 179
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TAG_SEQ=TGTAGCCGGG"
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cultivar="Salinas"
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CCCAAGCCCGCTCCGCTACGCCGCCTGGCCGCTGTACTGGATCGCGCAGGGGTGCG	Qy 72 IleProThrProLeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIle 91	Qy 52 ValHisAspLeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrTleProLeu 71	1701 AAGAAGGCCATCCCGCCACACTGCTTCGAGCGCTCGGTGCTCAAGTCCTTCTCGTACGTG	32 LYBLYBALAILeProThrHisCysPheGluArgSerVallleArgSerSerTyrTyrVal	Qy 13 GlyLysAsnIleLeuGluArgValProValAspProProPheThrLeuSerAspLeu 31 :::::: ::	76 (1-1794)	Mismatches: Indels: Gaps:	. No.: 1.52e-116 : 1049.50 ent Similarity: 63.53%	COASS.	velopmental stage" 3 LIBRARY"	/clone="ccmaa92" /tissue_type="Embryo"		rce	Email: trocherowiluc.edu Seq primer: M13 reverse. Seq primer: M13 reverse.	Tel: (217) 333-9643 Fax: (217) 333-9817	Torbert Rocherord University of Illinois 1102, S. Goodwin Ave., Urbana, IL 61801, USA	JOURNAL Unpublished (2001) COMMENT Contact: Dr. Torbert Rocheford	Mikkilineni, V. Genomic Organiz	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacelade; Panicoideae; Andropogoneae; Zea.	ldiplantae; Streptophyta;	S	B1683576/c B1683576 1.OCUS B1683576 1794 bp mRNA linear EST 31-DEC-2001 DEFINITION EST 01 B73 LIBRARY Zea mays cDNA clone ccmaa92 5', mRNA sequence. ACCESSTON B1683576	RESULT 7	220 ValLeuLeu 	655 AGGTTTGCCAACCACTTTGATCCCATGAGTCCAATTTTCACCGAGCGCGAGCGA	Qy 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGln 219	Db 595 AGGTTCACTCTAGGATTTCCTTTATACCTCTTAACTAATATTTCTGGCAAGAAATACGGA 654
SULT 8	Db 519 CAACAAG 513	570			Db 690 CTCTTCTCCACCATGCCGGCACTACCACGCCATGGAGGCCACCAAGGCGATCAGGCCCAT 631	750 ACTACGGCATCCTTCAACCGCGTGTTCCACAACATCACGGACACGCACG	Oy 295 spPheGlyPheLeu-AsnArgValPheHisAspValThrHisThrHisThleuHisHis 314	Qy 275 OHISTYFASpSerThrGluTrpAsnTrpIleLysGlyAlaLeuSer-ThrIleAspArgA 295	GATCGTGAACGCGTGGTGGTGCTCATCACCTACCTGCAGCACCCACC	255	235 @LeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIleProValLe	990	Qy 215 gGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLy 235	Db 1050 GCCGTACCCCGCGCTTCGCCTGCGCACTTCGGGACCCCTACGGCCCCATCTACAACGACCG 991	Qy 196 sLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspAr 215	Db 1110 CCCCCCCAATTTTTCTTTTTCGAAAGCCCGCTGTACCTGGCGAACGACGGCGTCGGGGGCG 1051	1169 - CGCGTTCCCCTTGGCAATTTCAACCCCCAAAGGGCCCCTTTTTAAAAAAAA	179 eArgLeuThrLeuGly		Oy 166 uleuAsnAsnProPro	159LysVallLysileTyrSerLysLe	Qy 150 uValTyrIleProLygArgLygSer		131 rTrpLysTyrSerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGl	Qy 112 LeuII1eAspAspI1eValGyPheValLeuHisSerAlaLeuLeuThr-ProTyrPheSe 131 :: :: :: ::	Db 1521 TGCACCGGCGTGTGGGTCATCGCGCACGAGTGCGGCCACCACGCCTTCTCGGACTACTCG 1462	Qy 92 LeuThrGlyLeuTrpVallleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGln 111

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Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
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CK269030.1 GI:39826008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Other_ESTs: EST715109
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        GluArgValProValAsp----ProProPheThrLeuSerAspLeuLysLysAlaIlePro
                                               GGAGCTGGTGGTCGTATGTCTGCTCCAATGGCGAGACTGAAGTA-AAGAAGAATCCTCTT
                                                                   GlyAlaGlyGlyArgMetSerAspPro----
                                                                                                                                                                                                                                                                                                                                                         grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and heat-stressed at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed stress was pooled to construct the CNNA library NAN sample "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construct the cDNA library. RNA sample."
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      Zea mays
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Other_GSSs: OGVHS09TH
Contact: Cathy Whitelaw
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                                                  LysGlyAlaAlaTrpValIleAsnMetTyrAlaIleProValLeuGlyValSerValPhe
                                                                                                         LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAlaAla
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                         TTCGGGTTCTGGTGGGTGCGCGCGTCTACGCCGTGCCGCTGGTGATTGTGAACGCGTGG
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/note="Vector:_pBCSK-; Site_1: HincII; 0.7-1.5
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CF098768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnollophyta; eudicotyledona; core eudicot asteridas; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.

1 (bases 1 to 611)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesebe Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Proj
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OHN8F08.yg.abi OH N sunflower H.argophyllus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://compgenomics.ucdavis.edu/
Unpublished (2002)
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helianthus
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ce: QHN8 row: F column:
                                                                                                /lab host="B.coli"
//lab host="B.coli"
/clone lib="QH_N sunflower H.argophyllus (drought stress)"
/clone="Vector: pGEM-T; The library was constructed from
three different sources (seedling, root and leaf) of RNA
from a single genotype. cDNAs were pooled and cloned into
a high-copy vector pGEM-T. Details of library constructior
can be obtained at http://cgpdb.ucdavis.edu/"
                                                                                                                                                                                                                                                                     /organism="Helianthus argophyllus"
/mol type="mRNA"
/db xref="taxon:73275"
/clone="QHN8F08"
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                   Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.
                                                                                                            1 (bases 1 to 869)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Ro Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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/clone lib="ZM 0.7 1.5KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/strain="B73"
/db_xref="taxon:4577"
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195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-24604
Fax: (204) 983-4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
Contact: Dr. Sylvie Cloutier
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Cloutier, S. and Fofana, B.
One Step RT-PCR on total RNA isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ail: scloutier@agr.gc.ca
e 'lin' sequences are derived
One Step RT-PCR on total RNA
                                                                                                                                                                                                                                                                                                                                                                                                              primer: M13 forward
                                                                                                                                                                                                                                                             Site_2: MluI; mRNA obtained flowering"
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|mol_type="mRNA"
|cultivar="AC McDuff"
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/dev_stage="12 days after
/lab_host="EMDH10B-TONA"
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960.00
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                        University of Saskatchewan, Department of Computer Science IC101 Engineering Building, 57 Campus Drive, Saskatcon, Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769
Fax: 306 966 2033
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Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gar
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gar
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Linke,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.
Functional Genomics of Abiotic Stress In Wheat and Canola unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parameters) has been run on this sequence. Lucy identified
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/mol_type="mRNA"
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
sasterids; lamiids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 963)
1 (bases 1 to 963)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
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EST716261 potato abiotic stress cDNA library
clone POACR59 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
Other_ESTs: EST716262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG_ACA CTA TAG.
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four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions
                                                                                                                                                                                                            /tissue type="abiotic stress treated leaf and root tissue"
/lab host="DH10B-TonA"
/clone lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
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clone="POACR59"
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                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
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  167
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Descurainia sophia
Descurainia sophia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.

1 (bases 1 to 1080)
Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J.,
Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Descurainia sophia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm,
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
  LeuAsnAsnProProGlyArgValPheThrLeuValPheArgLeuThrLeuGlyPhePro 186
                                         GAAAGAGATGAAGTCTTTGTCCCCAAGCAGAAATCTGCAAGTCAAGTGGTACGGCAAATAC
                                                            AspAsnAspGluValTyrIleProLysArgLysSerLysValLysIleTyrSerLysLeu 166
                                                                                                                      GTCCCTTACTTCTCTTGGAAATACAGTCATCGCCGTCACCATTCCAACACGGGTTCCCTC
                                                                                                                                        ThrProTyrPheSerTrpLysTyrSerHisArgAsnHisHisAlaAsnThrAsnSerLeu 146
                                                                                                                                                                                                    PheSerAspTyrGlnLeuIleAspAspIleValGlyPheValLeuHisSerAlaLeuLeu 126
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(613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       singhja@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 200C/16 hrs 1jht/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Ds01_13f05"
/tlssue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/clone_lib="Ds01_AAFC_ECORC_cold_stressed_Flixweed_seedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="mRNA"
db_xref="taxon:89411"
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Flixweed_seedlings
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287 GlyAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsnArgValPheHisAspVal 306
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                            932 GAGAAGAAAGGTGTGTACTGGTACAAC 958
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                                        GluHisLysGlyValPheTrpTyrHis 375
                                                                                                         AlaArgAspAlaIleLysProValLeuGlyGluTyrTyrLysIleAspArgThrProIle 346
                                                                                                                                                ThrHisThrHisValLeuHisHisLeuIleSerTyrIleProHisTyrHisAlaLysGlu 326
                                                                                                                                                                                                                                                                                                                                                 ProMetSerProIlePheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGly 226
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Search completed: June 23, Job time : 2383 secs

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